

GenCore version 4.5
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OM protein - protein search, using sw model.

Run on: September 4, 2002, 16:15:49 ; Search time 172.18 Seconds

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
472.225 Million cell updates/sec

Title: US-09-052-089A-2

Perfect score: 2393

Sequence: 1 MPILSLCTICSDPFDHSRDV..... VRKRTVSSASQPQLDTFLCQ 470

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%, Maximum Match 100%

Listing first 45 summaries

Database : SPTRREMBL 19;*

1: sp_archea;*
2: sp_bacteria;*
3: sp_fungi;*
4: sp_human;*
5: sp_invertebrate;*
6: sp_mammal;*
7: sp_mhc;*
8: sp_organelle;*
9: sp_phage;*
10: sp_plant;*
11: sp_rabbit;*
12: sp_virus;*
13: sp_vertebrate;*
14: sp_unclassified;*
15: sp_virus;*
16: sp_bacteria;*
17: sp_archaea;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT	1	ALIGNMENTS
ID	008854	
PREREQUISITE:		PRT;
AC	008854;	470 AA.
DT	01-JUL-1997 (TREMBL; 04, Last sequence update)	
DT	01-DEC-2001 (TREMBL; 19, Last annotation update)	
DE	MTRIP.	
GN	TRIP OR MTRIP.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
NCBI_TAXID=10090;		
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE:97238620; PubMed=9104814;	
RA	Lee S.Y., Lee S.Y., Choi Y.;	
RT	"TRAF-interacting Protein (TRIP): a novel component of the tumor necrosis factor receptor (TNFR)- and CD30-TRAF signaling complexes that inhibits TRAF2-mediated NF-kappaB activation.";	
RT	J. EXP. MED. 15:1275-1285(1997).	
RL	CC	-i - SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR	EMBL; U77844; AAB52994; 1;	
DR	MGD; MGI:1056377; Trapi.	
DR	InterPro; IPR001841; Znf_fingering.	
DR	Pfam; PF00097; zf-C3HC4; 1.	
DR	SMART; SM00184; RING; 1.	
KW	Zinc-finger.	
SEQUENCE	470 AA;	53191 MW;
SO	00FD705B52645133 CRC64;	
Query Match	96.7%;	Score 2315; DB 11; Length 470;
Best Local Similarity	97.7%;	Pred. No 4e-116;
Matches	459;	Conservative 0;
		Mismatches 11; Indels 0; Gaps 0;
Qy	1	MPILSLCTICSDPFDHSRDVAIHCGHFFHFLQLIQFETAPSRTCPQCRIQVKIIIN 60
Db	1	MPILSLCTICSDPFDHSRDVAIHCGHFFHFLQLIQFETAPSRTCPQCRIQVKIIIN 60

Q94987 drosophila
Q9qyt2 mus musculu
Q9qyt3 mus musculu
Q9h810 homo sapien
Q9xze3 ameba prot
Q26079 archaeoglob
Q9ibd4 gallus gall
Q9nj23 aequippecten
Q9nc13 drosophila
Q9eqn8 mus musculu
Q66878 aquifex aeo
Q90337 cyprinus ca
Q90338 cyprinus ca
Q92015 gallus gall
Q96720 dermatothiag
Q21440 caenorhabdi
Q9ips8 homo sapien
Q9hiq1 homo sapien
Q90338 cyprinus ca
Q26080 plaocpecten
Q9bwg0 homo sapien
Q63731 rattus norv
Q9vdz1 drosophila
Q961u3 drosophila
Q9nj22 aequippecten
Q9nj21 aequippecten
Q9nj20 aequippecten
Q97380 saccharomyce

QY 61 KLFDFLAQEENVLDAEFLKNEDSVKAQLSQDREKSDQAITDLRDLERNATES 120
Db 61 KLFDFLAQEENVLDAEFLKNEDSVKAQLSQDREKSDQAITDLRDLERNATES 120
QY 121 LQNALINKAEMCLCSTLKKONKFLEQRQDETQAREEAHRLCKMTMEQJELLIQSORSEV 180
Db 121 LQNALINKAEMCLCSTLKKONKFLEQRQDETQAREEAHRLCKMTMEQJELLIQSORSEV 180
QY 181 EEMIRDGMGVGOSAVEOLAVYCVSLSKEYNLKARKATGELADRKKLVSSSKLTN 240
Db 181 EEMIRDGMGVGOSAVEOLAVYCVSLSKEYNLKARKATGELADRKKLVSSSKLTN 240
QY 241 TELDOAKLELRSQDKLQSADEQETSLRKSDPPGPNLEPASATNETVSRLVFESPAVE 300
Db 241 TELDOAKLELRSQDKLQSADEQETSLRKSDPPGPNLEPASATNETVSRLVFESPAVE 300
QY 301 MMNIRLHQOPPGDEIDLNTFDVNTPPTQSGSCHPLPKLCLERARSFPMQVNLKKHV 360
Db 301 MMNIRLHQOPPGDEIDLNTFDVNTPPTQSGSCHPLPKLCLERARSFPMQVNLKKHV 360
QY 361 SKPESQLSAGGQRCVGELDEELAGAFPLTIRNAVYLQGOKPNRTAESAESRSTDVRYIGDD 420
Db 361 SKPESQLSAGGQRCVGELDEELAGAFPLTIRNAVYLQGOKPNRTAESAESRSTDVRYIGDD 420
QY 421 LGGRMKFIOPRDTTIRPVVKSKAKSKOKVRKTVSSASQPKLDTFLQ 470
Db 421 LGGRMKFIOPRDTTIRPVVKSKAKSKOKVRKTVSSASQPKLDTFLQ 470

RESULT 2

Q9CP4 PRELIMINARY; PRT: 470 AA.
ID Q9CP4
RC STRAIN="C57BL/6J"; TISSUE="EMBRYO";
RX MEDLINE=21085660; PubMed=11217851;
DT 01-JUN-2001 (TREMbrel. 17, Created)
DT 01-JUN-2001 (TREMbrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMbrel. 19, Last annotation update)
DE TRAF-INTERACTING PROTEIN.
GN TRAF1.
OS Mus musculus (Mouse).
OC Mammalia: Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RESULT 3

Q9BWF2 PRELIMINARY; PRT: 469 AA.
ID Q9BWF2
AC 0QBWF2;
RC STRAIN="C57BL/6J"; TISSUE="EMBRYO";
RX MEDLINE=21085660; PubMed=11217851;
DT 01-JUN-2001 (TREMbrel. 17, Created)
DT 01-JUN-2001 (TREMbrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMbrel. 19, Last annotation update)
DE TRAF-INTERACTING PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG CARCINOMA;
RA Strasberg R.;
RL Submitted (NOW-2000) to the EMBL/GenBank/DBJ databases.
CC !-! SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; BC00310; AAH00310.1; -.
DR InterPro; IP001841; Znf_ring.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; Sm00144; RING; 1.
KW Zinc-finger.
SQ SEQUENCE 470 AA; 53149 MW; EBRAFC49A9F4BF2E CRC64;

Query Match 96.4%; Score 2306; DB 11; Length 470;
Best Local Similarity 97.2%; Pred. No. 1..2..-115;
Matches 457; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 MPIISLCTCSDFDHRSRVAATHCGHTPHLOCLIQWFTAPSRCPCCRIOVGKTIN 60
Db 1 MPIRACTICSDFDHRSRVAATHCGHTPHLOCLIQWFTAPSRCPCCRIOVGKTIN 60
QY 121 LQNALINKAEMCLCSTLKKONKFLEQRQDETQAREEAHRLCKMTMEQJELLIQSORSEV 180
Db 121 LQNALINKAEMCLCSTLKKONKFLEQRQDETQAREEAHRLCKMTMEQJELLIQSORSEV 180
QY 181 EEMIRDGMGVGOSAVEOLAVYCVSLSKEYNLKARKATGELADRKKLVSSSKLTN 240
Db 181 EEMIRDGMGVGOSAVEOLAVYCVSLSKEYNLKARKATGELADRKKLVSSSKLTN 240
QY 241 TELDOAKLELRSQDKLQSADEQETSLRKSDPPGPNLEPASATNETVSRLVFESPAVE 300
Db 241 TELDOAKLELRSQDKLQSADEQETSLRKSDPPGPNLEPASATNETVSRLVFESPAVE 300
QY 301 MMNIRLHQOPPGDEIDLNTFDVNTPPTQSGSCHPLPKLCLERARSFPMQVNLKKHV 360
Db 301 MMNIRLHQOPPGDEIDLNTFDVNTPPTQSGSCHPLPKLCLERARSFPMQVNLKKHV 360
QY 361 SKPESQLSAGGQRCVGELDEELAGAFPLTIRNAVYLQGOKPNRTAESAESRSTDVRYIGDD 420
Db 361 SKPESQLSAGGQRCVGELDEELAGAFPLTIRNAVYLQGOKPNRTAESAESRSTDVRYIGDD 420
QY 421 LGGRMKFIOPRDTTIRPVVKSKAKSKOKVRKTVSSASQPKLDTFLQ 470
Db 421 LGGRMKFIOPRDTTIRPVVKSKAKSKOKVRKTVSSASQPKLDTFLQ 470

RESULT 4

Q9CP4 PRELIMINARY; PRT: 470 AA.
ID Q9CP4
RC STRAIN="C57BL/6J"; TISSUE="EMBRYO";
RX MEDLINE=21085660; PubMed=11217851;
DT 01-JUN-2001 (TREMbrel. 17, Created)
DT 01-JUN-2001 (TREMbrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMbrel. 19, Last annotation update)
DE TRAF-INTERACTING PROTEIN.
GN TRAF1.
OS Mus musculus (Mouse).
OC Mammalia: Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RESULT 5

Q9BWF2 PRELIMINARY; PRT: 469 AA.
ID Q9BWF2
AC 0QBWF2;
RC STRAIN="C57BL/6J"; TISSUE="EMBRYO";
RX MEDLINE=21085660; PubMed=11217851;
DT 01-JUN-2001 (TREMbrel. 17, Created)
DT 01-JUN-2001 (TREMbrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMbrel. 19, Last annotation update)
DE TRAF-INTERACTING PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG CARCINOMA;
RA Strasberg R.;
RL Submitted (NOW-2000) to the EMBL/GenBank/DBJ databases.
CC !-! SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; BC00310; AAH00310.1; -.
DR InterPro; IP001841; Znf_ring.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; Sm00144; RING; 1.
KW Zinc-finger.
SQ SEQUENCE 469 AA; 53294 MW; B9EF3808FBC5985B CRC64;

Query Match 76.3%; Score 1836.5; DB 4; Length 469;
Best Local Similarity 77.6%; Pred. No. 4..3..-90;
Matches 363; Conservative 41; Mismatches 63; Indels 1; Gaps 1;
InterPro; IP001841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00144; RING; 1.

TRAF interacting protein.

Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi;
Actinopterygii; Neopterigii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
NCBI_TaxID=31033;
RN [1];
SEQUENCE FROM N.A.
MEDLINE=914B33; PubMed=10025966;
RA Cottage J., Clark M., Hawker K., Umrania Y., Wheeler D., Bishop M., Elgar G.;
RA three receptor genes for plasminogen related growth factors in the genome of the puffer fish Fugu rubripes. ";
RL FEBS Lett. 443:370-374(1999).
CC -I SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
EMBL: AA03177; CA09084 1; -
DR InterPro: IPR01841; zf_ring.
DR SMART: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger.
SEQUENCE 433 AA; 49201 MW; A8C31AAA4216EBC2 CRC64;

Query Match 38.4%; Score 919; DB 13; Length 433;
Best Local Similarity 40.7%; Pred. No. 8.8e-42;
Matches 191; Conservative 87; Mismatches 117; Indels 74; Gaps 6;
QY 1 MP1SLCTCSDFDHSRVAIAHGHTFLQCLIQWETAPSRTCPOCRQVGKTTIN 60
DB ||| :||||||||||||||||||||||:||||:||||:|||:|||:|||:|||:|||:
QY 61 KLFEDLAOBEEVNLDAEFLKNEELDSVKAQDOKREKRSDQSAILDTLRTDEERNATES 120
DB |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
QY 61 RLYRDVGUDSSVGDPESIQLNEDLRVKWNFSKKERDWREKOKAMODLMEVELQRKALEN 120
DB |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
QY 121 LQNLANKKAMCSTLKKFLQEORQDTEKQAREAHRLCKKMKTMEQIELLOSRSEV 180
DB |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
QY 121 LOKYMEKEKRLCSALRTQMYLESOHNDTRAKKEEVRRRLRKMTKFESLDVLOGRAEV 180
DB |||:|||:|||:|||:|||:|||:|||:|||:|||:
QY 181 EEMIRDGMGQOSAVEQALAVYCUSLKKEYENLKEAKATGEGLADRIKKDLVSSRSKLTN 240
DB |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
QY 181 ESMITDMGIGQAAYEOLSTIVCISLRKEYDNLKGKLSSNEMCEKLRREVLTNSNHLHKAL 240
DB |||:|||:|||:|||:|||:|||:|||:|||:|||:
QY 241 TEJDQAKLERSAQDKLQGADQETTSLRKKSDDPGPNLEPASATNETVSRLVFESPAVE 300
DB |||:|||:|||:|||:|||:|||:|||:|||:
QY 241 LETLKARDMKSLONDLTNAKEISSLKKVFEFLOEAISPTRTNEALGRLLFERGAAP 300
DB |||:|||:|||:|||:|||:|||:|||:
QY 301 MMNR-----LHOPPFGEIBIDLNTTFDNPPTPQTSGSQHCLPLKRLRARSPKQNVL 354
DB |||:|||:|||:|||:|||:|||:|||:
QY 301 PONSRVSKASCLHPPSGNEDIDLNMVTPD-----DVRKRKPVPS 344
DB |||:|||:|||:|||:
QY 355 KKHHVKVKSESOLSLGGQRCVGELDEELAGAPFLIRNAVLGOKPNRRTAESRSSTDVV 414
DB |||:|||:|||:|||:
QY 345 KKKH-----LDSVV-----TLLRTKKNLVSNOGK----FV 371
QY 415 RIGFDGLGGRTKETQPRDTTIRPVPKSKAKSKOKVRKVIVSSASOPK 463
DB |||:|||:|||:|||:|||:
QY 372 QSGYDGIGGRTKIFQPRTHAVR-----SEASKPE 401
DB |||:|||:
RESULT 7

Query Match 11.8%; Score 281 5; DB 5; Length 455;
Best Local Similarity 22.0%; Pred. No. 8.6e-08;
Matches 106; Conservative 99; Mismatches 197; Indels 79; Gaps 50;
QY 7 CTICCSDFDHSRVAIAHGHTFLQCLIQWETAPSRTCPOCRQVGKTTINLFFDL 66
DB 6 CVCIAELFGQADEWFATVGHMFHNCLNQWLDR--SKTCPOCRNKTCTRNIF-RVYFNL 62
QY 67 ADERFENVLDAEFLKNEELDSVKAQDOKREKRSDQSAILDTLRTDEERNATESLNALN 126
DB 63 ANLUDVSHIDVGSLQEQDNLAMSLSKMKVERKNDQEQIRDLKETOKKCLKTIAGLEOKVO 122
QY 127 KAEMLCSTLKKFLQEORQDTEKQAREAHRLCKKMKTMEQIELLOSRSEVEMIRD 185
DB 123 KKDPLISSYVEQGVLKSDAHWVTLGRKENKTKLTSQIOSMEGISTSILAGSADADRLL 182
QY 187 MGVGOSAVEQALAVYCUSLKKEYENL---EARATGELADRIKKDLVSSRSKLTNT- 241
OS Drosophila melanogaster (Fruit fly).
OS Diptera; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OS Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydriidae; Drosophilidae; Drosophila.
OC Fugu rubripes (Japanese pufferfish).
OC NCBI_TaxID=7227;
RN [1];
SEQUENCE FROM N.A.
STRAIN=BERKELEY;
RN MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananatode P.G., Scherer S.E., Li P.W., Hostkins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers R.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.I.G.,
RA Abril J.F., Agbayani A.B., An H.-J., Andreadis P., Brannoch C., Baldwin D.,
RA Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Boishakhy S.,
RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Brodtier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahake R., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew A.T., Dietz S.M.,
RA Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov L., Dunn P.,
RA Durbin R.J., Ewanilesta C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howard T.J., Wei M.-H., Ibebewam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Nobarry C., Morris J., Mohrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacelli J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Purvi V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svartkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassaman D.A., Weinstein G.M., Weissbach J., Yao W.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA RT "The genome sequence of Drosophila melanogaster.";
RA Science 287:2185-2195(2000).
CC -I SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMAIL: ARGO3800; AA5F7730; -
DR FlyBase: FBgn034314; CG5140.
DR InterPro: IPR018181; zf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger.
SEQUENCE 455 AA; 50726 MW; BEA74F4ACE8FD5B CRC64;

Db	183	---EADPHVLANWWSTKRELROCESKKTTELNVVKVQNDRKEELKRYHANNIPNV	238
Qy	242	-----ELDQAKLRLSA--OKDQSADEITSURKKS---DPPGNLEPASATNEVSR	290
Db	239	FIDMCSFDCSKLBERVSHLESOLYQAEKLQAFENKITYLDSP---NASCGLNNTILA	294
Qy	291	LVPE----SPAPVEMMPRLHQPPGSEDEIDNTFDVNTPPTQTSQSQCICPKK--LC	342
Db	295	IKEBERRTTISPYKENT-----RIESTSPVNI-KSSVGLAHLLNTKGNING	343
Qy	343	LEBAR-SPMONVKKVHKVSKPSQLSLLGGQRCVGEDELALAGAFLFIRNAVLGOKOPN	401
Db	344	LASKISKPIKGVGGVSMTS-----GTIRKISSSDLSEKYSIF-----KRPR	384
Qy	402	RTEAESRSTDVWRIG---FDGLGGRKFIFORDTIRPVVPSKAKSKQVKRITKVSS	457
Db	385	LLIGGSSSSALTATGNSNFVNGMGSEK-----VDPEFAQREEBGLSTIRSSTAL	435
Qy	458	S 458	
Db	436	S 436	
RESULT 8			
ID	Q95SS5	PRELIMINARY; PRT; 435 AA.	
AC	Q95SS5;		
DT	01-DEC-2001 (TREMBlrel. 19, created)		
DT	01-DEC-2001 (TREMBlrel. 19, last sequence update)		
DT	01-DEC-2001 (TREMBlrel. 19, last annotation update)		
DE	GH03577P.		
GN	CG3140.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metaboa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Daptera; Brachycera; Muscomorpha;		
OC	Ephydriidae; Drosophilidae; Drosophila.		
OX	NCBI_TAXID=7277;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN^Y, CN BW SP;		
RA	Stepleton M., Broststein P., Hong L., Agbayani A., Carlson J.,'		
RA	Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,'		
RA	Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,		
RL	Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AX060610; ADZ28158.1; -.		
DR	SEQUENCE 435 AA; 48455 MW; 08FF0AC81DD9416E CRC64;		
RESULT 9			
ID	Q9M143	PRELIMINARY; PRT; 506 AA.	
AC	Q9M143;		
DT	01-OCT-2000 (TREMBlrel. 15, Created)		
DT	01-OCT-2000 (TREMBlrel. 15, Last sequence update)		
DT	01-DEC-2001 (TREMBlrel. 19, last annotation update)		
DE	PURININE RING ZINC FINGER PROTEIN.		
GN	AT1G01270.		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eurosidids II; Brassicales; Brassicaceae; Arabidopsis.		
OX	NCBI_TAXID=3702;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Lamari B., Stoetzing T., Stumpf J., Mewes H.W., Lemcke K.,		
RA	Mayer K.F.X.;		
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.		
CC	RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AL161491; CAB80936.1; -.		
DR	InterPro: IPR001841; Zinc_fing.		
DR	Pfam: PF00097; zf-C3HC4; 1.		
KW	Zinc-finger; SMART; SM00184; RING; 1.		
SQ	SEQUENCE 506 AA; 56518 MW; 1B06751A4E299FEB CRC64;		
Query Match			
Best Local Similarity	11.7%	Score 280.5; DB 5; Length 435;	
Matches	164;	Conservative 99; Mismatches 187; Indels 83; Gaps 17;	
Qy	7	CTCSDFDHSRVAIHCHTHLOCUTQWFETAPS---RVCPCQRIQVKKTINKLFFDL	66
Db	6	CVTCALFGQADEVEATVGHMFHNCLNQWLDR---SKTCPOCRNKCT'RNTRF-RVYFN	62
Qy	67	AQEENVLADEFKLNDSVKAQLSQKREKRQSAITDLRDTLEERNATESLQNALN	126
Db	63	ANDVSHDVGSSQEQOLNAMLSMKMVKEKNDEQQIDLKTKQKLTQKLTIGLEQKVQ	122
Qy	127	KAEMCSTLKKQMKFLEQRDETQAREBAHRICKMKTMEQFELLQSORSHVEEMRD	186
Db	123	KKPLLISSVYEQGVLKSDAHVVDGLRKENKTKLKSQOSMEGQSAILAGSAPADRLLK	182
Qy	187	MGYGQSAVEQOLAYCVCUSLKEYENLK---EAKKATGELADRKKKDVYSSRSLKTLWEDQAKL	239
Db	183	---EADPHVLANWWSTKRELROCESKRTRELKRLKLEERVSHL	238
Qy	240	NTELDQAK-----LELRSAQKDLOSADEITS-LRKSSDDPPGPNLEPASATNETVSRV	292
Db	239	ESDLYQAEQEKLOAFENKTYLDSPPNASCGLNNSNIALKREERUTISP--TVKENIKR-I	295
Qy	293	FESPAPVEMMPRLHQPPGEGDEIDLNTTFDVNTPTQTSQSOHCLPKK--LCLEAR-SP	349
Db	296	BESTSPY-----LNT-----KSSVGLAHLNTRGNIGLAKSRS	331
Qy	350	MQNLUKKHHKVSKPESQSLGGQRCVGLDEELAGAFLFIRNAVLGOKPRTTAERS	409
Db	332	IKGVGGYSMTS-----GTIRKISSDLSEKYSIF-----KPRUILLGSSS	372
Qy	410	STDVVRIG---FDGLGGRKFQIOPRDTTIRPVVPSKAKSKQVKRITKVSS	458
Db	373	SALTATSSNFVNGMGSEK-----VDPEFAQREEBGLSTIRSSTALS	416
Query Match			
Best Local Similarity	9.2%	Score 221; DB 10; Length 506;	
Matches	120;	Conservative 79; Mismatches 193; Indels 156; Gaps 24;	
Qy	5	SLCTCISD---FDHDHSRVAIHCHTHLOCUTQWFETAPS---RVCPCQRIQVKKT	57
Db	10	AICSCICYEDLKPVYENLQOSISA--CGHVPHELCQWFCYCPSTNKRNCIPCKOKCSLD	67
Qy	58	LIINKLFFDIAQEENVL-----DAEFLKNELDKWAQL---SOKDRKRSOAI	104
Db	68	PCRLYFOSSGNOTDISIASPKWVGIEEDPVWFLKQVLCRKYKLGKVKLQNLKOMKFLQRODDETQCAR	127
Qy	105	DTLRDTLEERNATESLQNALNKAEMLCKLKKMFLQRODDETQCAR	154
Db	128	DKLHQCNQELKEDKVKRWEALQEISTQHILKUKSECQIQLNSQCVQIER--TVALAK	184
Qy	155	EARHLLKC-----KHMTCBDEIELLQOS---ORSEVEEMR--DMGV	189
Db	185	ELASLKLVSDLSLEDDVVLKALLGNNAKTMKTDTDLVYSLVIRNSRKYKELAKCNGOLGR	244
Qy	190	GQS-AVEQDLCVYSLKEYENLKEAKKATGELADRKKKDVYSSRSLKTLWEDQAKL	248
Db	245	GARSSEKSKLEKALEKTIKKRMRELEETRERENBALRNDIVNS--KCSYEVSEPAI	301
Qy	249	ELRSAQKDLOSADEITS-LRKSSDDPPGPNLEPASATNETVSRVLFESPAPVEMMPRLQ	308
Db	302	ESMSFRML---SSDNKV---EKISTPPGKLEEKDGFTIQGSCL-----RGRE	343

QY 309 PPFGDEIDLNNTFDVN--TPPTQPTSG-----SQHCLPKKLCLEARSPMQNV 354
Db 344 DSVSRTD--SVIVDYYDPETNTSGIRDWNTNIEKGDNMSVKDKINRKPDTSSV- 400
QY 355 KKVHKVKSPESQO-----ISLGGORCVG-----ELDEELAGAFPLFIRNVLGQK 399
Db 401 -----SPYSNGSGNIWOSGSGTNRNLGRWSKHKGERNEATPSLGGSP----- 441
QY 400 PNRITAESRSSTDVWRIGEGLGKTFTOPRDTLIRVPUKSKAKSO-----KVRI 453
Db 442 -----RKDDLISIGPGGGIK-----VLRKPOQTKTNAASSGSKRFKLT 484
QY 454 KVNSASQ 461
Db 485 KTSGSSQ 492

RESULT 10
P9090 PRELIMINARY; PRT; 425 AA.
AC P9090; DT 01-MAY-1997 ("REMBrel. 03, created)
DT 01-MAY-1997 ("REMBrel. 03, Last sequence update)
DE B0432.9 PROTEIN.
GN B0432.9.

OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderrinae; Caenorhabditis.
OX NCBI_TAXID=6239;
RN [1]
RC STRAIN=BRISTOL N2;
RX MEDLINE=94150718; PubMed=7905398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laiister N., Larreille P.,
RA Lightning J., Lloyd C., Murray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Riffken L., Roopra A., Saunders D., Shownkeen R.,
RA Smalton N., Smith A., Sonnhammer E., Straden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Spratt J., Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans".
RL Nature 360:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Henkhaus J., Wohldmann P.;
RT "The sequence of C. elegans cosmid B0432.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
CC -I- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; U08836; AAB37893.1; -.
DR InterPro; IPR00181; Znf-finger.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
DR Zinc-finger.
SQ SEQUENCE 425 AA; 48104 MW; 375F524F5C092B2D CRC64;

RESULT 11
Q9Q284 PRELIMINARY; PRT; 2473 AA.
ID Q9Q284; AC 09Q284; DT 01-MAY-2000 ("REMBrel. 13, Created)
DT 01-MAY-2000 ("REMBrel. 13, Last sequence update)
DE B0432.10 PROTEIN.
GN LEKL (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TAXID=10890;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99303227; PubMed=10373470;
RA Goodwin R.L., Pabon-Pena L.M., Foster G.C., Bader D.;
RT "The cloning and analysis of LEKL identifies variations in the
LEK1/centroneure protein F-milosin gene family.".;
RL J. Biol. Chem. 274:18597-18604(1999).
DR EMBL; AF194970; AAC07196.1; -.
DR MGDB; MGTR191546; 65304A22Rik.
FT NON_TER 1
SQ SEQUENCE 2473 AA; 1 281903 MW; 504E91A1A150A3ES CRC64;

Query Match 8 5%; Score 204.5; DB 11; Length 2473;
Best Local Similarity 20.5%; Pred. No. 0.0063; Matches 95; Conservative 101; Mismatches 163; Indels 105; Gaps 14;

QY 56 KTIINKLFFDLAQEEN---VDAEFLKNELDPSVKAQLSQKDREKDSQATIDTLRTL 111
Db 1629 KDTVETLERELERSBENOBAILDSNELENKAEVETLAKOQDEMFKSLRIFELDLVTRER 1688
QY 112 EERNAVTESELQNALANKAEMCLSTKKOMPFEDR-----QDEWKOAREAA 156
Db 1689 ENLAKOLOKQKRSVSELDLRRCSLRLRKEEQLQMLQKLRELREV 1748
QY 157 HRLKCKMKMMEQIELLOSSQRSEVEEMRDMGVQOSAVELAVYCUSVKKKEYENLKEER 216
Db 1749 AALCNDQETIKAQFQSLSDPGPGEVHHL-----KSSIRKLKVHIDAEKKHQNILEQK 1801
QY 217 ATGELADRIK-----KDLV----SSRSKLTNLTDQARKEELRSAQKDL- 257
Db 1802 ESKHHADLKDVRVENLEQELLSERKNMFOAEKSKEIQTLLKSEIORMAQNLQDQBLI 1861
QY 258 --QSADEQETSLRKSKDPPGPNLEPASATNETVSR-----LVFESPPAPVMMPHLH 307
Db 1862 STRSENENLKLKEQEVRSVDLITNPNSIENLKDKEQVKONKEEAKITVEMQLOTLK 1921
QY 308 OPPFGDEIDLNNTFDVNPTPQTSGOSHCLPKKLCLEARSPMQNVLKVVHKVKSPSQL 367
Db 1922 -----ELNETV-----VSLCNDQ-----EVSKTEQ- 1942

Query Match 8 5%; Score 204.5; DB 5; Length 425;
Best Local Similarity 25.9%; Pred. No. 0.001; Mismatches 73; Conservative 49; Indels 105; Gaps 12;

Db 724 QIOLKESTIQQLA-----KONELE-DEQKKQSESEVHIOEIKQNTQKDFELVESGES 777
 Qy 104 IDTLRDTLEERNATVESLQANLANKAEMLCSTLKKMK-FLEQRODETQAREEARHLCK 162
 Db 778 LKKLQOOLEOKTGLHEKLQALEE-----LKKERETIKEKEOLOOLQSRSASESA 830
 Qy 163 MKTME-QIELLQOSRESEVEMTRMGVGOSAVOLAVIC---VSLKEYENL---KE 213
 Db 831 LKVWQVOLELOQOQQAASGEGEBSVAKLHDEISOLKSQAEETOSELKSTFOSNLEAKSKO 890
 Qy 214 ARKATGELADRIKKD-LVSSRKLTNLTELDQAKLERSAQDLSAQDQTSLRKKS 271
 Db 891 LEAANGSLEEAKNSKGHLQQTICK---SEVGEQAAQALSSCHTDVESKIQ 939
 Qy 272 DDPGNLEPASATNETVSRLVFESPA-----PVEMMNPRLHQ 308
 Db 940 -----LEANALALEVKNEYAESREASDQLQDKVEITDLHAELQAERSSSALHTKL 993
 Qy 309 PPFGBEI-----DNTTDFDNTPTQTSQHSCPKKKLICERRASPMQ 351
 Db 994 SKFSDEIATGHKELTSKAD-----ANSQMLQKEKELOELRQOLOPSODDSQTKLAE 1045
 Qy 352 -----NVLKVKVKVSKPESQSLGQRCVGELDEELAGAFLFIRAVLGOK 398
 Db 1046 GERKERSKSFEEISKNIQEEVTKAKTENLEPLSTGTQPTIKQERLE-----ITVAELQIK 1099
 Qy 399 QPNRTAESAESSSTDVVRIGFDGLGRTKFQPRD-TTIRPVPKSKAKSKQVKYIKTVS 457
 Db 1100 -----EKMASEDAQKIA-----DJKTULVERAOVANANTISATNAELSTVL 1138
 Qy 458 SASQ 461
 Db 1139 EVLQ 1142

RESULT 14

007569 PRELIMINARY; PRT; 2139 AA.

ID Q07569; 002504; ID 094932; PRELIMINARY; PRT; 2017 AA.

AC DT 01-NOV-1996 ("REMBrel. 01, Created)
DT 01-JUL-1997 ("REMBrel. 04, Last sequence update)

DT 01-DEC-2001 ("REMBrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN.

GN Entamoeba histolytica.
OS Entamoeba; Entamoebidae; Entamoeba.

NCBI_TaxID=579;
RN [1] SEQUENCE FROM N.A.

RC STRAIN=HMT; IMSS;
RX MEDLINE=93295430; PubMed=8515774;

RT "Identification of a myosin heavy chain gene (mhc) from the human parasitic pathogen Entamoeba histolytica.",
Mol. Biochem. Parasitol. 59:123-131(1993).

RN Raymond-Denise A., Sansonetti P., Guillen N.;
RT SEQUENCE FROM N.A.

RT SEQUENCE FROM N.A.

RA Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.

DR EMBL; U03534; AAB4065.1; -.

DR HSSP; P08799; 1MND; InterPro; IPR00148; IQ.

DR InterPro; IPR001609; myosin_head.

DR Pfam; PF00612; IO; 2.

DR Pfam; PF00653; myosin_head; 1.

DR PRINTS; PR00193; MOSTINHEAVY.

DR SMART; SM00242; MSc; 1.

SQ SEQUENCE 2139 AA: 245225 MW: C68307341DB51DD1 CRC64;

Query Match

8.0%; Score 191.5; DB 5; Length 2139;

Best Local Similarity 22.1%; Pred. No. 0.027; Index 97; Gaps 16; Matches 97; Conservative 83; Mismatches 161; Indels 97;

Matches 97; Conservative 83; Mismatches 161; Indels 97; Gaps 16;

Qy 6 LAQEENVNLDAEFLKNELDSVKAQLSQ-----DREKRSQAIIDTIRDTLEERNATV 118
 Db 1671 VAQEERK---ORJESDIAKLEQEERTAAEAEKKRTOELEKFNLDVTNR 1726
 Qy 119 ESL--ONALANKAEMLCSTLKKQMFLEQRODETQAREEARHLCKMKTNEQIELLQSQ 176
 Db 1727 EKLVAKNSENDAET--DSKKEKKALE--DEIEKITDNRNLS----EEDSLDRK 1775
 Qy 177 RSEVEMIRUNGVGOSAVOLAVICVSLIKKEYENLKEARKATGELADRKKDLYSSRL 236
 Db 1776 NALLDSKDSVSMKERFODELKVTKDALTEKHNHAETWRKG---RLEKEAEVQVRL 1831
 Qy 237 KTLNTELDQAKLERSAQDLSAQDQETTSIRKKSDDPPGQNLEASATNETVSRLVFESP 296
 Db 1832 EAQNLDNLQAKQEKATKRAAGDGEELSLMNEELDDVBDLQDQLD 1876
 Qy 297 APVEMMNPRLHQPPGDEIDNTAFD-----VNTPPTOTSGSOHCPLPKCLE----R 345
 Db 1877 -----ODDLADKELADLTDQKTKLVIQKSVDSRIO-MQQLDLEKAGRK 1924
 Qy 346 ARSPHMNVLKVKVSKPESQ-----SLGSGRCVGELDEELAGAFLFIRNA 393
 Db 1925 NOKOKAYEKKLOQENDNDFEEYKETADKRIVNLSAQK-DDQKEL-----EK 1973
 Qy 394 VLQKOPNRTAE-----SRSSTDVVRGFQDGGRKTFIOPRDTITRVPVSKAKS 447
 Db 1974 ERGLKQDSEKEVORLVKQOLETKVAEG--GANVSIKVKVAKAYEAETEELT'EAEDAL 2031
 Qy 448 KOKVRIKTTSSASQPKLD 465
 Db 2032 KAKMKAEKAKTSQKLD 2049

RESULT 15

007569 PRELIMINARY; PRT; 2017 AA.

ID 094932; PRELIMINARY; PRT; 2017 AA.

AC 094932; 024138; ID 094932; PRELIMINARY; PRT; 2017 AA.

DT 01-FEB-1997 ("REMBrel. 02, Created)
DT 01-FEB-1997 ("REMBrel. 02, Last sequence update)

DT 01-FEB-2001 ("REMBrel. 19, Last annotation update)
DE NONMUSCLE MYOSIN-II HEAVY CHAIN.

GN ZIP OR CGI5792.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;

OC Pterygota; Neoptera; Tracheata; Diptera; Brachycera; Muscomorpha;

OC Ephdroioidea; Drosophilidae; Drosophila.

OC NCBITaxID=7227;

RN [1] SEQUENCE FROM N.A.

RP MEDLINE=9514335; PubMed=8568878;

RA Mansfield S.G., al-Shirwi D.Y., Ketchum A.S., Newbern E.C., Kiehart D.P.:

RT "Molecular organization and alternative splicing in zipper, the gene that encodes the Drosophila non-muscle myosin II heavy chain." J. Mol. Biol. 255:98-105(1996).

DR EMBL; U35816; AAB03051.1; -.

DR HSSP; P10587; 1BR2.

DR Flybase; FBgn005634; zip.

DR InterPro; IPR000048; IQ.

DR InterPro; IPR001609; myosin_head.

DR InterPro; IPR004008; Myosin_N.

DR InterPro; IPR02928; Myosin_tail.

DR Pfam; PF00612; IO; 1.

DR Pfam; PF00653; myosin_head; 1.

DR Pfam; PF02736; Myosin_N; 1.

DR Pfam; PF01576; Myosin_tail; 1.

DR PRINTS; PR00193; MOSTINHEAVY.

DR SMART; SM00015; myosin_head; 1.

DR SMART; SM00015; IQ; 1.

DR	SMART; SM00242; MSC; 1.	RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
DR	PROSITE; PS50096; IQ; 1.	RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ikegami C.,
SEQUENCE	2017 AA; 232089 MW; 8C76FF2EBD02E8E CRC64;	RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kannison J.A., Ketchum K.A.,
QY	56 KTINKLFFLDAQEENVIDAE~FLKNELDSVKAQLSQRDRKRSQ~-----AI 103	RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Db	1263 KTVI[EK]-----AKTGLEAENDADLATERLSVNSRRENDRRQKAQSIAELQVKLAE 1314	RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
QY	104 IDTDLRDTLEER---NATVESLQNALNKAEMLCSTLKKOMKFHQDQETKOREEHR- 158	RA	Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
Db	1315 IERARSELQEKCTKLQOEAEIN[NOLEEAELKASA]AVKSASNNESOLTEQAQLEETRQ 1374	RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Mosheri A.,
QY	159 --LKCKMKTMEQIELLOSQRSEVEEMTRDMVGQSAVEQLAVYCVSILKEVNLFAR 215	RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Db	1375 KLGSSKLQIESEKEALQEOLQEEDEAKRN Y--ERKIAEV[T]QMEIKKKAAEDADLA 1431	RA	Nelson D.R., Nelson A.N., Nixon K., Nusskern D.R., Paclob J.M.,
QY	216 KAGELADRLKKDVSSRSKLTKL---NTELDOAKLERSAQD---LQSADQEITSIR 268	RA	Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Db	1432 KELEGGKKRNLKDIEALERQVKEIJAQNDRLLDKSKKQSOELEDATIELEAQTKVLE 1491	RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
QY	269 KKSDPPGNEPASATNEVSRVLYFESPAPVMNRPHQPPDQEIDLT[D]VNPPT 328	RA	Shue B.C., Siddon-Klamo S., Simpson M., Skupski M.P., Smith T.,
Db	1492 KKQK---NFEDKTLAEEKAISEQTAQERDTAEREAREKETKVLSVRELD[AD]---- 1541	RA	Sper E., Spradling A.C., Stapleton M., Strong R., Sun E.,
QY	329 QTGSQHCLPKKCLERAPS[P]MQL-----KVKVHKSP---ESOLIS-LGGQ 372	RA	Svistekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Db	1542 -----KIEDLENKRTLQNEELDDLANTOCTADKVNHELEKAKRALESQALELKAO 1591	RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
QY	373 RCVGELDEEL 382	RA	Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Db	1592 N-[E]ELEDDL 1599	RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RESULT	16	RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
ID	Q9WQB8	RT	"The genome sequence of <i>Drosophila melanogaster</i> ,"
AC	Q9WQB8	DR	Science 287:2185-2195 (2000).
DT	01-MAY-2000 (TREMBrel. 13, Last sequence update)	DR	EMBL; AE003465; AA#47311.1; -.
DT	01-MAY-2000 (TREMBrel. 19, Last annotation update)	DR	HSSP; PI0587; 1BR2.
DE	ZIP PROTEIN	DR	Flybase; FBgn0050534; zip.
GN	ZIP OR CG15792.	DR	InterPro; IPR000048; IQ.
OS	Drosophila melanogaster (Fruit fly).	DR	InterPro; IPR011609; myosin_head.
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;	DR	InterPro; IPR004009; Myosin_N.
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	DR	InterPro; IPR002928; Myosin_tail.
OX	Ephydriidae; Drosophilidae; Drosophila.	DR	Pfam; PF00612; IQ; 1.
NCBI_TAXID=7277;		DR	Pfam; PF02736; Myosin_N; 1.
RN	[1]	DR	Pfam; PF01576; Myosin_tail; 1.
RP	SEQUENCE FROM N.A.	DR	PRINTS; PR00193; MYOSIN_NEAV.
RC	STRAIN=BERKELEY;	DR	PRODOM; PD00355; myosin_head; 1.
RX	MEDLINE=2016006; PubMed=10731132;	DR	SMART; SM00015; IQ; 1.
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hostins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champs M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Heit L., Nelson C.R., Miklos G.I.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S., Borikova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtsik C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin R.K., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fosler C., Gabril A.E., Garg N.S., Gelbart W.M., Glaser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,	DR	SEQUENCE; PS50096; IQ; 1.	
Q9WQB8	PRELIMINARY;	PRT:	2056 AA.
Q9WQB8	PRELIMINARY;	PRT:	2056 AA.
QY	55 KTINKLFFLDAQEENVIDAE~FLKNELDSVKAQLSQRDRKRSQ~-----AI 103	Db	1302 KTVI[EK]-----AKTGLEAENDADLATERLSVNSRRENDRRQKAQSIAELQVKLAE 1353
QY	104 IDTDLRDTLEER---NATVESLQNALNKAEMLCSTLKKOMKFHQDQETKOREEHR- 158	Db	1354 IERARSELQEKCTKLQOEAEIN[NOLEEAELKASA]AVKSASNNESOLTEQAQLEETRQ 1413
QY	159 --LKCKMKTMEQIELLOSQRSEVEEMTRDMVGQSAVEQLAVYCVSILKEVNLFAR 215	Db	1414 KLGSSKLQIESEKEALQEOLQEEDEAKRN Y--ERKIAEV[T]QMEIKKKAAEDADLA 1470
QY	216 KAGELADRLKKDVSSRSKLTKL---NTELDOAKLERSAQD---LQSADQEITSIR 268	Db	1471 KELEGGKKRNLKDIEALERQVKEIJAQNDRLLDKSKKQSOELEDATIELEAQTKVLE 1530
QY	269 KKSDPPGNEPASATNEVSRVLYFESPAPVMNRPHQPPDQEIDLT[D]VNPPT 328	Db	1531 KKQK---NFEDKTLAEEKAISEQTAQERDTAEREAREKETKVLSVRELD[AD]---- 1580
QY	329 QTGSQHCLPKKCLERAPS[P]MQL-----KVKVHKSP---ESOLIS-LGGQ 372	Db	1581 -----KIEDLENKRTLQNEELDDLANTOCTADKVNHELEKAKRALESQALELKAO 1630
QY	373 RCVGELDEEL 382	Db	1631 N-[E]ELEDDL 1638

RESULT	17		
ID	094987	PRELIMINARY;	PRT; 2057 AA.
AC	094987;		
DT	01-FEB-1997 (TREMBLrel. 02, last sequence update)	Created)	
DE	01-DEC-2001 (TREMBLrel. 19, last annotation update)	NONMUSCLE MYOSIN-II HEAVY CHAIN.	
GN	ZIP OR CG15792.		
OS	Drosophila melanogaster (Fruit fly)		
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oxymerida; Drosophilidae; Drosophila.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=9614635; Pubmed=8568878;		
RA	Mansfield S.G., al-Shirawi D.Y., Ketchum A.S., Newbern E.C., Kiehart D.P.;		
RT	"Molecular organization and alternative splicing in zipper, the gene that encodes the Drosophila non-muscle myosin II heavy chain."; J. Mol. Biol. 255:91-109(1996).		
RL	255:91-109(1996).		
DR	EMBL: U35016; AAC09049.1;		
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DR	FlyBase; FBgn0005634; zip.		
DR	InterPro; IPR000048; IQ.		
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DR	Pfam; PF00063; myosin_head; 2.		
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DR	Pfam; PF01576; Myosin_tail; 1.		
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DR	ProDom; PD000355; myosin_head; 1.		
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DR	SEQUENCE; PS50096; IQ; 1.		
RX	2057 AA; 236642 MW; 0D59519C1EB3A411 CRC64;		
RA	Matsumura S.; Me2a/Golga3 Gene Product is Indispensable for Spermatogenesis in the Mouse. " Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.		
RT	Mouse. ";		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AB029537; BA86890.2; -.		
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DT 01-MAY-2000 (TREMblrel. 13, Created)			
DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)			
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)			
DE MALE ENHANCED ANTIGEN 2/GOLGI AUTOANTIGEN, GOLGIN SUBFAMILY A, 3.			
GN ME2/Z-GOGLG3.			
OS Mus musculus (Mouse)			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX NCBI_TaxID=10090;			
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SEQUENCE FROM N.A.			
RP STRAIN=57BL6;			
RC			
RA Matsukuma S.;			
RT Mez/Golga3 Gene Product is Indispensable for Spermatogenesis in the Mouse. ";			
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.			
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Query Match 7.9%; Score 189.5; DB 11; Length 1487; Best Local Similarity 22.7%; Pred. No. 0.023; Matches 95; Conservative 77; Mismatches 158; Indels 89; Gaps 16;			
QY 65 DLAAQEEENVLDA-EFLKNE-----LDSVKAQLSKDREK-----DSQIIDIITRD 109			
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Db 812 DLAVKSNQVEHQOE-----TATLRQMQVKKEQFLQKVNAVEAYRDAKDQLINE 864			
QY 152 ARGEAHRIKCKMKTMEQIELLQOSRSEV---EMTRDMGVQOSAVEQDLYCVSLKKE 207			
Db 865 LKATKKRDLSEMELBQLQELIKQLEKKTVEHEHSRQLQMSLVHQMAELEGHLQSYOKE 924			
Qy 208 YEN-----LKEA---RKATGBLADRIKKDLYSSRSKLTKNTTELDOA 246			
Db 925 RDPMEIHKQSLKDFKEQMLALTANETIKKQFELQEQAKKATEQOKKMKRGSUTSA 984			
Qy 247 KLEIRSAQDKLQASAOETTSRKKRSDDPGNLIPASATNETVSRLVFESSPAPYMMNRL 306			
Db 985 QKSMKTHKAYENA--VSILSRLOEA--LASKEATDAELNQLRAOSTG--GSSDPVL 1036			
QY 307 ROPPFGEIDLNTT-----FDVNTPPTGSGS-OHCLPKKICLERRSPMO--NV 357			
Db 1037 HEKTRALEVELQNGQSKILLERELQEVITMTSQELEESREKYLEDELQESRGFRKI 1096			
Qy 358 HKYKSPQESLSGGQRCWGELEDLAGEPFLFTRNAVLGQKQNRNTAESRSSTDWII 416			
Db 1097 KRIBESNKKLAL-----ELEHERGKLTLGQSNSNALREHNSILETALAKREADYLQ 1148			
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AC Q9X83;			
DT 01-Nov-1999 (TREMblrel. 12, Created)			
DT 01-Nov-1999 (TREMblrel. 12, Last sequence update)			
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)			
DE CDNA LUJ13615 FIS, CLONE PLACE1010895, WEAKLY SIMILAR TO NUFL PROTEIN.			
OS Homo sapiens (Human)			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TaxID=9606;			
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SEQUENCE FROM N.A.			
RP STRAIN=57BL6;			
RC			
RA Matsukuma S.;			
RT Mez/Golga3 Gene Product is Indispensable for Spermatogenesis in the Mouse. ";			
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.			
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QY 153 REAEHRLKCKMKT-----EQTEFLLIQSQSERVEEMTRDMGVQOSAVEQ 196			
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QY 48 QCRIQVGKTTINKL-----FFLQAEQEEENYDAEFTKLNEQDSVKAQLSKDREKDSQALID 105			
Db 80 QAKFENQIQTKVMLNELEMAGOSAGGRDTFRFLNEICQOLEKOLEQDRELEDEMEKEL 139			
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Db 140 KEKKVNEQDQLALRBEAENENNSKRNRENKRKKNNEQDQDIDYQKQDSKETLUR 199			
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Db 200 EDSYRSQISLKNYELIQVLDIQTLTNEANEKTFEVONEMRKLEESVOEM----- 250			
QY 197 LAVVCVSLKKEYNLKEARKATGELADRKK-----DLYSSRSK-----LKT 238			
Db 251 -----EKMDDEYNRMKATWHTQDNDVQDQLKKENDHYQLQVQELTDLKSKNEEDDPINVA 305			
Qy 239 LNTFLDQAKLLELSAQKQDQSOEITSRKKSDDPGNLPEASATNETVSRLVFESSPAP 298			
Db 305 VNAKVNEENLILUSKSKDDEIYEQMLHNREKLN-----AQLDACKNSVNVLAQOGIQRDQ 363			
Qy 299 VEMMNPRLIQKOPPDEIDINTTF-----DVNTPPPTGSGSCHLPKKLCLERRSPMO---NV 353			
Db 364 IKMITEQVEQ---YIKEMERNTCIEDLNKLNLORNIGA-----STLSQTHMIQSTLDI 415			
Qy 354 LKKYHVSKSPESOLSLGCGCVCGLDEDELLAGA 385			
Db 416 LKETKTEARTAELAEDAR--EKDKELVEA 444			
RESULT 21			
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ID Q9X83			
AC Q9X83;			
DT 01-Nov-1999 (TREMblrel. 12, Created)			
DT 01-Nov-1999 (TREMblrel. 12, Last sequence update)			
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)			
DE MYOIN HEAVY CHAIN.			
OS Amoeba proteus (Amoeba).			

OX Eukaryota; Lobosea; Gymnamoebia; Amoebidae; Amoeba.
 NCBI_TaxID=5775; [1]
 RT Characterization of myosin heavy chain and its gene in Amoeba
 prot.;
 J. Eukaryot. Microbiol. 45:600-605(1998).
 RP SEQUENCE FROM N.A.
 RC STRAIN=D; MEDLINE=99082369; PubMed=9864850;
 RA Oh S.W., Jeon K.W.;
 RA "Characterization of myosin heavy chain and its gene in Amoeba
 prot.;"
 RA Submitted (MAR-1999) to the EMBL/GenBank/DDJB databases.
 RN [2]
 SEQUENCE FROM N.A.
 RC STRAIN=D;
 RA Oh S.W., Jeon K.W.;
 RA Submitter (MAR-1999) to the EMBL/GenBank/DDJB databases.
 RN EMBL: AF136711; AAD3718.1;
 DR HSP; P08799; BMD.
 DR InterPro; IPR000448; IQ.
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 DR Pfam; PF02736; Myosin_N; 1.
 DR PRINTS; PR0193; MYOSINHEAVY.
 DR PRODOM; PDO00355; myosin_head; 1.
 DR SMART; SM00242; MYSC; 1.
 DR SEQUENCE 2138 AA; 24427 MW; DB5BBB308639FA71 CRC64;

Query Match 7.9%; Score 188.5; DB 5; Length 2138;
 Best Local Similarity 22.2%; Pred. No. 0.039; Mismatches 170; Indels 119; Gaps 17;
 Matches 102; Conservative

QY 56 KTIINKLFDIAQEEENVNLDAEFLKNELDSVKAQLS----- 92
 Db 1247 KKLVARLKESDKMKKEKEYEDERDKLNKDAQ-KLSQLADEDLKNALEEMAKNRSEKEN 1305

QY 93 -KDREKR----DSQAIITDL-----RTDTLEERNATVESLONALNKAEMLCSTL 135
 Db 1306 RKKLENRLRELEQDGAARSNSLEKKFRGFEDNLHDQSYDEVQDDVNVLSAAKKKL 1365

QY 136 KKOMKLEQRODETKQAREEHLRKCKMKTW---QIELLQSQRSEVEEIRDMVGQ 191
 Db 1366 ESELEALKRSRDLNEAEGRKVAEE--KMKVLTDELHBLQALSLNAENKNTGLVRNVKVO 1422

QY 192 SAVEQLAVCVSLKKEYENLKEARKATGELADRLLKKDLVSSRSKLKTINTEDQAKELL 251
 Db 1423 DEVEDLINEQLENASKELSKLDKGNKTEAKELRHHVQESQ-----SDAGEKLKR 1475

QY 252 SAQDKLQSOADEETSLRKKS-----DPGPGLNLEPASATNETVSLRVFESPA 297
 Db 1476 HTQDELDELHOLEAKSSLERSKKQLOLQVDDLEDTHEELAARTKAERLVKOLEA 1535

QY 298 PV-EMNNPRUHQPPFCD-----EIDL-----NTTF----- 323
 Db 1536 DLAELQETRESEPLMQAELKSLLEVLDLKKDADRSOFAKVENERSALEYEDL 1595

QY 324 NTPPQTOS--GSQHCLPKL-----CLERASPMQVNLKKHVSKPESOLSIG 371
 Db 1596 QAQDGETSKILANARRAKKUNTDLDEQSLKLEKASNAQSKLEKRLKKAAKAS 1655

QY 372 ORCVGEL-DIEEL--AGAFPLFTRNAVYLQKOPNRTAESP 408
 Db 1656 ARAGGGVSDEELRRRAOAELAALRDDA-DERSNSNLTAEK 1694

RESULT 22
 028714 PRELIMINARY; PRT; 1156 AA.
 AC 028714; 01-JAN-1998 (T-EMBLrel. 05, Created)
 DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)

DN 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
 DE CHROMOSOME SEGREGATION PROTEIN (SMC1).
 GN NCBI_TaxID=2234;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=86049343; PubMed=938975;
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Lofus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
 RT The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.;
 RL Nature 390:364-370(1997).
 DR EMBL: AE000995; AAB89690.1; -.
 DR TIGR: AF1558;
 DR InterPro; IPR003439; ABC_transporter.
 DR InterPro; IPR003405; SMC_C.
 DR InterPro; IPR002017; Spectrin.
 DR Pfam; PF024483; SMC_C; 1.
 DR PROSITE; PS00311; ABC_TRANSPORTER; UNKNOWN_1.
 KW Hypothetical protein; Complete proteome; Sequence 1156 AA; 134244 MW; 18CB167CD5AD1ED CRC64;

Query Match 7.8%; Score 186.5; DB 17; Length 1156;
 Best Local Similarity 16.7%; Pred. No. 0.026; Mismatches 18; Indels 125; Gaps 1; Matches 78; Conservative

QY 55 KTTINKLFDIAQEEENVNLDAEFLKNE----- 82
 Db 671 KERMISDKTYVLOREKEGLFAELNRAESLRKROYKEDVDRLLGTMITSERNRNRLSLLPEKIRT 730

QY 83 -----DSVQAQLSQDREK-----RDSQAIIDTLRDTLEERNATVESLONALNKAEML 131
 Db 731 ESGRIEELRKISOKRSREKENYISSIKDVKNSLAMEAEIGELEAIEEIERMLGSE-- 788

QY 132 CSTLKKOMKLEQRODETKQAREEHLRKCKMKTW---BOIELLQSQ-----RSEV 180
 Db 789 --VFKIVEELDKTKEEHORNREILISIERSKIESLEFKREOLESSMKEQVYLDEIKDR 845

QY 181 EEMPRDMGVQGSQAVFELAVCVSLKKEYENLKEARKATGELADRKKDLVSSRSKLTN 240
 Db 846 DEIRTRIEGKARVEEINSEELLEKKEERELGKLRKERDELJNOKRKE 905

QY 241 TELODQAKLERSAQDLSQDQEITSLRKSKDDPPGNLLEPASATNETVSLRVFESPA 300
 Db 906 AEIJURERERIKLQKERELEAESETKEIGEV-EVENLPLEPKVVLDEV----- 955

QY 301 MMNPRLHQPPFGEDDLNTFDFWNPPTO-----TSGSQHCLPKKICLERARSPMQLVK 355
 Db 956 -----VELSTPGDVNLKAOEYEEVAKRDRDELVEKKMVKLEKERA---DILD 998

QY 356 KVHKVSKPSQLSLGGQRCVGEDELAGAFLFTRNAVYLQKOPNRTAESPSSDVVR 415
 Db 999 RIERVEMRKEI-----FFEVF-----TAINRNRAEIR 1027

QY 416 IGFPIGLGGKTFIOPRTTIRPVVKSKRASKVKRIVKVSQ 461
 Db 1028 --ELANGSGELYLSDDPFNSGIKIKVPPNPKVQKLSMSGGER 1070

RESULT	23	Db	1274 --OSOKSRLQAE
026079		09IBD4	1284
ID		PRELIMINARY;	PRT; 1937 AA.
026079		09IBD4	PRELIMINARY;
AC		09IBD4	PRT; 1937 AA.
01-NOV-1996	(TREMBrel. 01, Created)	01-NOV-1996	(TREMBrel. 01, Last sequence update)
DT	01-NOV-1996	01-DEC-2001	(TREMBrel. 19, Last annotation update)
DT	01-DEC-2001	01-DEC-2000	(TREMBrel. 15, Last sequence update)
DE	MYOSIN HEAVY CHAIN.	01-DEC-2001	(TREMBrel. 19, Last annotation update)
OS	Placopecten magellanicus (Sea scallop);	01-DEC-2001	(TREMBrel. 19, Last annotation update)
OC	Bivalvia; Metacoda; Mollusca; Bivalvia; Pteriomorpha; Pectinoida;	01-DEC-2001	(TREMBrel. 19, Last annotation update)
OC	Pectinoidea; Pectinidae; Placopecten.	01-DEC-2001	(TREMBrel. 19, Last annotation update)
RN	[1]	01-DEC-2001	(TREMBrel. 19, Last annotation update)
RP	SEQUENCE FROM N.A.	01-DEC-2001	(TREMBrel. 19, Last annotation update)
RC	TISSUE=SKELETAL MUSCLE;	01-DEC-2001	(TREMBrel. 19, Last annotation update)
RA	Perreault-Micale C.; Kalabokis V.; Nyitrai L.; Szent-Gyorgyi A.G.;	01-DEC-2001	(TREMBrel. 19, Last annotation update)
RT	"Sequence variations in the surface loop near the nucleotide binding site modulate the ATP turnover rates of molluscan myosins.";	01-DEC-2001	(TREMBrel. 19, Last annotation update)
RL	J. Muscle Res. Cell Motil. 0:0-0(1996).	01-DEC-2001	(TREMBrel. 19, Last annotation update)
DR	EMBL: U59244; ARB03660.1; -.	01-DEC-2001	(TREMBrel. 19, Last annotation update)
DR	HSSP; P24733; IMNCI.	01-DEC-2001	(TREMBrel. 19, Last annotation update)
DR	InterPro; IPR00048; IQ.	01-DEC-2001	(TREMBrel. 19, Last annotation update)
DR	InterPro; IPR01609; myosin_head.	01-DEC-2001	(TREMBrel. 19, Last annotation update)
DR	InterPro; IPR004009; Myosin_N.	01-DEC-2001	(TREMBrel. 19, Last annotation update)
DR	InterPro; IPR002928; Myosin_tail.	01-DEC-2001	(TREMBrel. 19, Last annotation update)
DR	InterPro; IPR02017; Spectrin.	01-DEC-2001	(TREMBrel. 19, Last annotation update)
DR	InterPro; IPR00612; IQ; 2.	01-DEC-2001	(TREMBrel. 19, Last annotation update)
PFAM	PF00063; myosin_head.	01-DEC-2001	(TREMBrel. 19, Last annotation update)
DR	PF02736; Myosin_N; 1.	01-DEC-2001	(TREMBrel. 19, Last annotation update)
DR	PF01576; Myosin_tail; 1.	01-DEC-2001	(TREMBrel. 19, Last annotation update)
DR	PRINTS; PR00193; MYOSINHEAVY.	01-DEC-2001	(TREMBrel. 19, Last annotation update)
DR	PRODOM; PD00035; myosin_head; 1.	01-DEC-2001	(TREMBrel. 19, Last annotation update)
DR	SMART; SM00015; IQ; 1.	01-DEC-2001	(TREMBrel. 19, Last annotation update)
DR	SMART; SM00242; MYSC; 1.	01-DEC-2001	(TREMBrel. 19, Last annotation update)
DR	PROSITE; PS50096; IQ; 1.	01-DEC-2001	(TREMBrel. 19, Last annotation update)
SEQUENCE	SEQUENCE FROM N.A.; 1941 AA; 223243 MW; E2AD1637FFDB8127 CRC64;	01-DEC-2001	(TREMBrel. 19, Last annotation update)
Query Match	7.7%; Score 184; DB 5; Length 1941;		
Best Local Similarity	22.4%; Pred. No. 0_061; Mismatches 131; Indels 134; Gaps 19;		
Matches	97; Conservative		
QY	55 KTTTINKLFFD--LAQEENNVLDAEFLKNEELDSVK--AOLSQ 92		
Db	906 EKLIMOKADFEQQIKELEERLIDEEADASDLEGIGKMMEDGDNANLKKDIGELEHSLQKSE 965		
QY	93 KDFEKRSQATIDL-----RDTLEERN-ATVESLQ----NALNA 128		
Db	966 QBAHKDNO--ISTLOGEMSODDEHIGKLNLKEAKKTSDSQAEDKCNHLNK- 1022		
QY	129 EMKCSTLKKMFFLEQRODQETKQAREFAHLKCKMK---TMEQIELLQSQRSEVEEM 183		
Db	1023 -LKAKLEQALDELDNEREKKVGVKEAKSKVGEQDLKSQIENEDLERVRR-ELEEN 1079		
QY	184 TR-----DMGVQOSAVEQLAVYCVSLSKEYENLKEARKATGELADRLLKDVSS 232		
Db	1080 VRKKEAETTLNSKLEDEQNLVSQORKIKELQARIEELEELAEARNARKVQRAEL 1139		
QY	233 RSKLKTNTLEDDQ-----KLERSAQKDQSA-----DQETSLRKSDPP 274		
Db	1140 NRBLEELGERLUDBAGGAIISAQIELNKREAEELKIRDRDLEASLQHEAQISAIRKKHD- 1198		
QY	275 PGNLEPASATNETVSLRVFESPAVPEMNPRJHQPPGDEIDLNTFDVNIPPTQSGSQ 334		
Db	1199 -----AANIMADQV-----DQLOQVKSKIEK---DKKQKREND---DLSQMT 1236		
QY	335 HCLPKKICLERRSPMNVLKVVKVHPKSPESOLSLGGQRCVGELDELAGAFLPLFRMLGOKPN 401		
Db	1237 HDWKNGCSEKVKQFES-----QVSDLNARLE-DSQRSINEL----- 1273		
QY	395 LGOKPNRTAES 407		
Query Match	7.7%; Score 183.5; DB 13; Length 1937;		
Best Local Similarity	20.4%; Pred. No. 0_065; Mismatches 165; Indels 59; Gaps 11;		
Matches	78; Conservative		
QY	59 INKLFEDLAQEEENVL--DAEFLKNEELDSVKQOLSQKDRERKSDQAITDRLTLERNA 116		
Db	1267 MTRLMNDLTQTKLQSENGEFVR-QLEEKESSLISQLSQRGTSFTQOIELRQLFEEK 1325		
QY	117 TVESLQNALNKAEMLCITLKKQMKFLEQRQDETQKOREEAHRLKCKMTMQIOELLQSQ 176		
Db	1326 SINALAAQARHDCILURQEOYEERQEEAKSALQRALSKQNAEVAWRTKETDQTE 1385		
QY	177 RSEVEEMTRDMGV---GQSAVEQLAVYCVSLSKEYENLK-----EARKATGELADR 224		
Db	1386 -- ELEDAAKKLKAARLQEAEEATEANAKCSSELEKTHRLQNELEDMDILKRAASL 1443		
QY	225 LKDLVSSRSKAKLN--TELDQAKLERSQKQDQSOADOBITSLRKSDPPGNLEPA 281		
Db	1444 DKK---QRGFDKLINDWQKQYEEQSRELAQSLSTBLFKLKNAYEFLDILETL 1499		
QY	282 SATNETVSLRVFESPAVPEMNPRJHQPPGDEIDLNTFDVNIPPTQSGSQ 341		
QY	1500 KRENKNQEEISLDLNTQISESGNLH-----EIE-----KVKVOEQESEVQL 1543		
Db	1544 ALEEAEGALEHESKTLRFOLESOLKADFERKLAKADEMENI-----RRNQO 1592		
QY	402 RT-----TAERSSTDVVR 416		

Db	1593 RTIDSQSLDSEARSRNAIL 1615	OY	389 FIRNAVLGOKQPNRRTAESRSST 411
RESULT	25	PRELIMINARY:	PRT: 1219 AA.
09N023	09NJ23	PRELIMINARY:	PRT: 1219 AA.
AC	09N123;	09N13	PRELIMINARY:
DT	01-OCT-2000 (TREMBrel. 15, Created)	ID	09N13
DT	01-OCT-2000 (TREMBrel. 15, Last sequence update)	AC	09N13;
DE	01-DEC-2001 (TREMBrel. 19, Last annotation update)	DT	01-OCT-2000 (TREMBrel. 15, Created)
GN	MYOSIN HEAVY CHAIN STRIATED MUSCLE SPECIFIC ISOFORM (FRAGMENT).	DT	01-DEC-2001 (TREMBrel. 19, Last annotation update)
MHC	Aequipecten irridians (Bay scallop).	DE	01-DEC-2001 (TREMBrel. 19, Last annotation update)
OC	Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Pectinoida;	DE	MUD PROTEIN.
OC	Pectinidae; Argoppecten.	DR	MUD PROTEIN.
OX	NCBI_TaxId=31199;	DR	Drosophila melanogaster (Fruit fly).
RP	[1] SEQUENCE FROM N.A.	DR	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
RX	MEDLINE=20090924; PubMed=106233517;	DR	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
RA	"Catchin", a novel protein in molluscan catch muscles, is produced by	DR	Hydrozoa; Drosophilidae; Drosophila.
RT	alternative splicing from the myosin heavy chain gene.";	OX	NCBI_TaxId=7227;
RL	J. Mol. Biol. 295:169-178 (2000).	RN	[1]
EMBL:	AF083905; AF062391.1; -.	RP	SEQUENCE FROM N.A.
DR	HSSP: P4733; IWDG.	RA	Mushroom body defect, a gene involved in the control of neuroblast
DR	InterPro: IPR00048; IQ.	RL	proliferation in Drosophila, encodes a coiled-coil protein.";
DR	InterPro: IPR001609; myosin_head.	RA	Proc. Natl. Acad. Sci. U.S.A. 97:8122-8127(2000).
DR	InterPro: IPR002938; myosin_tail.	RP	[2]
DR	InterPro: IPR002017; Spectrin.	RA	SEQUENCE FROM N.A.
DR	InterPro: IPR000533; tropomysosin.	PRado A., Raabe T.;	Prado A., Raabe T.;
DR	Pfam: PF00612; IQ; 2.	DR	Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
DR	Pfam: PF00063; myosin_head; 1.	DR	EMBL; AF20906; AF089163.2; -.
DR	Pfam: PF01576; Myosin_tail; 1.	DR	Flybase; FBgn002873; mud.
DR	PRINTS: PR00194; TROPOMYOSIN.	SQ	SEQUENCE 1871 AA; 216126 MW; AE3BE89F9937F76D CRC64;
DR	PRODOM: PD00355; myosin_head; 1.	DR	SMART: SM00015; IQ; 1.
DR	PROSITE: PS50096; IQ; 1.	FT	PROSITE: PS50096; IQ; 1.
SQ	SEQUENCE 1219 AA; 141202 MW; BAC6F574DA4AFBBBB CRC64;	FT	NON_TER 1
Query Match	7.6%; Score 183; DB 5; Length 1219;	Query Match	7.6%; Score 181.5; DB 5; Length 1871;
Best Local Similarity	23.0%; Pred. No. 0.042; Mismatches 102; MisMatches 102; Conservative 67; Indels 146; Gaps 20;	Best Local Similarity	22.0%; Pred. No. 0.08; Mismatches 144; Indels 67; Gaps 11;
QY	55 KTTTINKLFFD-----LAQEEENVIDAELTNEELDSVKAQL-----SO 92	QY	56 KTII--NLFLDQAEEENVLD-AEFLKNEELDSVKAQL-----REK 97
Db	184 EKLIMQKADPESQIKELEERLILDEADAADLEGSKKKHADNANLKKDGDILENTLOKA 243	Db	1243 KSVIEAQTLKSLDDQREBSAQQLVNDKVELKERLQVNSAFEAQTKLSDDLOREK 1302
QY	93 KDRERKDSQAIITPL-----RDTLEERN-ATVESLQ-----NALNKA 128	QY	98 RDQSAIDLTDLTDEERNATVESIQLNAKEMCSTIKKOMFKLEQRDETQKAREAH 157
Db	244 QDKAHKDNO---ISLFOGEISQDQEHHIGKLNEKAKALEANKKTSDSLQAEEDCNHLNK- 300	Db	1303 ESAQQLVDNLKVLDKERLQVSKVIAQOTKLSDDQREBSAQQLVNDKVELK 1356
QY	129 EMACSTLKKMQLEROQDETKEAREEAKRKKMK----TWEQIELLQSOSREVEEM 183	QY	158 RLKCKMKTMEQIELLQSOSREVEEMIRMGVSQASAVEQAVICVSLKKEYNLKEARKA 217
Db	301 --DKAKLQDQALDELDNEREKRKGVEAKKRVQEQLKSIQDENVEBLVR-ELLEN 357	Db	1357 ELDKERKEALKVSKVIAEQTQLSDQREBSAQQLVNDKVELKERLQVNSAFEA 1416
QY	184 TR-----DMGVGSQASQVOLAVCVSLKEYENKEAKRKGATGELADRKKDLVSS 232	QY	218 TGELADRKDKDVSSRSKKTLMWDLQDKAKLERSAQAKDLSQADQETSLRKSDDPGN 277
Db	358 VRKKEAEISSLNSNKSLEQDQNLYSQLQRIKELQARIELEEELEAERNARAKKEVKQRAEL 417	Db	1417 QTKLSDDQQRQKESAQQLVNDKVELKERLQVNSAFEAQTKLSDD-----1465
QY	233 RSKLKTLMELDQA-----KLELRSQAKLQSA---DOEITSRKSDPP 274	QY	278 LEPA SATNETVSRVLVFESPAVPEVMNPRLQPPFGDEIDLNTFDVNTPPTQSGSQ 337
Db	418 NRSELLEGLERDLFAGGATSAQIHLNKKRKEAELLRKIRRDLLEASLQHEAOISALRKHH- 476	Db	1465 ---LECQRESWQDVLNPKVLEKKELEAK-----VNSAFEAQTKLSDD-----L 1504
QY	275 PGKLEPASATNETVSRVLVFESPAVPEVMNPRLQPPFGDEIDLNTFDVNTPPTQSGQ 334	QY	338 PKKLCLERARSPMQLVKKVHKVSKPESOS-----LGRCYQGELDEELLAGRPL 386
Db	477 -----AAANEADQV-----DLOQKVKSKLEK---DKDKLREMD---DLESQMT 514	Db	1505 SDDLKLOKEDAQREVFVLYVERLYKEFREEVKLTLEDIELTLEMRCT-OMEERATAY 1562
QY	335 HCLPKKKLCLERARSPMQLVKKVHKVSKPESOS-----LGRCYQGELDEELLAGRPL 388	QY	Mus musculus (Mouse).
Db	515 HNNKNKGSEK-----VMQK-----ESQMSDNARLEDSQSRSTNL----- 551	QY	
RESULT	27	Q9EON8	
ID	09EON8	PRELIMINARY:	PRT: 324 AA.
AC	Q9EON8;	AC	Q9EON8;
DT	01-MAR-2001 (TREMBrel. 16, Created)	DT	01-MAR-2001 (TREMBrel. 16, Last sequence update)
DT	01-MAR-2001 (TREMBrel. 16, Last annotation update)	DT	01-JUN-2001 (TREMBrel. 17, Last annotation update)
DE	MITOIN (FRAGMENT).	DE	MITOIN (FRAGMENT).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Qian M.; Lin D.; Zhu X.;
 RT "Evolution of the internal repeat of mitosin.";
 RL Submitted (Sep-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP182407; AAG43426.1; -.
 DR InterPro; IPR00533; Tropomosin.
 DR PRINTS; PR00194; TROPOMOSIN.
 FT NON_TER 324 324
 SQ SEQUENCE 324 AA; 37896 MW; A64CD5A55E1DFD7 CRC64;

Query Match 7.6%; Score 181; DB 11; Length 324;
 Best Local Similarity 21.4%; Pred. No. 0.014; Mismatches 106; Indels 58; Gaps 9;
 Matches 65; Conservative 75; Mismatches 106; Indels 58; Gaps 9;

QY 56 KTIINKLFLDLAGQEEN---VILDAEFLKNEEDSVKAQLSKRSKREKRDSQASITDTLRTL 111
 Db 25 KDKVVENLERELEMSEENOELAIDSLENKAEVETLKAQDMEMAKSLRVFELDLVNVRSE 84

QY 112 EEPNATATESLQNLANKAEMLCSTLKKM-----KFLEROQDETQARBEAHR-----LKCKM 163
 Db 85 ENLAQOLQEKPSVSELDELCSLL-----SLSSEKEQARVOMERUDSKSAMLMLOT 137

QY 164 KTM-EQBLI----LQSQRSEVEEMIRDGMVGQSAVEQALAWYCVSILK---YENLK 212
 Db 138 KEWEEVAALVNQDQETIKAQEQSLDQGEEVILKSSIQKLKHADKKKCHILEQLK 197

QY 213 EARKATGELADR-----KRDVL---SSRSKLTNTLEDOAKELRSAOK 255
 Db 198 ESKHHADLFKDRVENLEOELMUSKEKNKEHLFQAENSKRAEIQTLTEQTMONLQDEL 257

QY 256 DIQSDQDGETSURKKSDDPGNGNEPASATNEWSRIV-----FESSAPVEMNP 304
 Db 258 ELNTNSREBKENLMKLNKEQOJSKLETINSSIERLLKDKEQKVQVKVKEEARITVEMLQT 317

QY 305 RLHQ 308
 Db 318 QLKE 321

RESULT 28

ID 066878 PRELIMINARY; PRT; 1156 AA.

AC 066878;
 DT 01-AUG-1999 (TREMBlre. 07, Created)
 DT 01-AUG-1998 (TREMBlre. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBlre. 19, Last annotation update)
 DE CHROMOSOME ASSEMBLY PROTEIN HOMOLOG.
 GN XCP_C OR AQ_629.

OS Aquifex_aerofluces

OC Bacteria; Aquificales; Aquificaceae; Aquifex.

OX NCBI_TAXID=63363;
 RN [1]
 RP STRAIN=IP5;

RC MEDLINE=98106666; PubMed=9337320;
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aufay M., Huber R.,
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex_aerofluces.";
 RL Nature 392:353-358(1998).
 DR EMBL; AP00599; AAC0339.1; -.
 DR InterPro; IPR003439; ABC_transporter.
 DR InterPro; IPR001687; ATP_GTP_A.
 DR InterPro; IPR003715; RNA_Polymerase.
 DR InterPro; IPR003405; SMC_N.
 DR InterPro; IPR003395; SMC_N.

RESULT 29

ID 090337 PRELIMINARY; PRT; 1933 AA.

AC 090337;
 DT 01-NOV-1996 (TREMBlre. 01, Created)
 DT 01-NOV-1998 (TREMBlre. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBlre. 19, Last annotation update)

DE MYOSIN HEAVY CHAIN.

OS Cyprinus carpio (Common carp).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Buteleosteii; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Cyprinus.

OX NCBI_TAXID=9622;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=FAST SKELETAL MUSCLE;

RC MEDLINE=9732533; PubMed=9208928;

RA Hiayama Y., Watabe S.;
 RT "Structural differences in the crossbridge head of temperature-associated myosin subfragment-1 isoforms from carp fast skeletal muscle.";
 RT "cDNA cloning of myosin heavy chain isoforms from carp fast skeletal muscle and their gene expression associated with temperature acclimation.";
 RT "Exp. Biol. 200:27-34 (1997)."
 RL J. Exp. Biol. 200:27-34 (1997).
 DR EMBL; D89990; BAA22067.1; -.

DR InterPro; IPR002017; Spectrin.
 DR Pfam; PF02483; SMC_C; 1.
 DR Pfam; PR02463; SMC_N; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 1156 AA; 135563 MW; B12B30F70C0CE49 CRC64;

Query Match 7.6%; Score 181; DB 16; Length 1156;
 Best Local Similarity 20.1%; Pred. No. 0.051; Mismatches 141; Indels 88; Gaps 16;
 Matches 81; Conservative 92; Mismatches 141; Indels 88; Gaps 16;

QY 66 LAQEEENV---LDAEFLKNEEDSVKAQLSKRSKREKRDSQASITDTLRTL 111
 Db 207 LKEKEKELEKEFQLRKRETEAKILLKEKEKLKRERUNELSSIRELESLEDITQIQ 265

QY 120 SLQNALNKAEMLCSTLKKM-----KFLEROQDETQARBEAHR-----LKCKM 171
 Db 266 ENKEKELNERERLIKKEVNEKIMPKEKVKCFKAETEAEKEREKELKESENVRVKLE 325

QY 172 LIQOSORSEVEEMIRDGMVGQSAVEQALAWYCVSILK---YENLK 212
 Db 362 ERKVKRELEEEERBKLTTFDEVKLEEKEKLTPEKLNKEOEL--EIOPANLNKE 419

QY 286 --ETVSRVLFESPPAV----EMMNPLRHQPFGEDEIL-NTFDVNTPPTGSQH 335
 Db 420 RIKEKDINKLISEREKIKEIKEKEQETKRIKAKTKKEEEELRNLTQELNLYEKR--- 473

QY 336 CLPKKLCKCERARSPPMONTLKKVVKVSKRESQSLSGGQRCCVGEDELAGAFLFIRNAVL 395
 Db 474 -----LSEVRKKELEVKLGAIEREWRSFS-----DVSDFVKD1KGVYGSV- SELI 519

QY 396 GQKPNRITTAESKSSTDWWRIGDGLGGRTKEQPRTDTIIR 437
 Db 520 RVKRNPEHITA-----IEVAG-SGRLKFTIVWDEBEVAK 550

DR	EMBL; D50474; BAA09067.1; -.	RC	SEQUENCE FROM N.A.
DR	HSSP; P13547; 2MYS.	RA	TISSUE=ADUCTOR MUSCLE;
DR	InterPro; IPR000048; IQ.	RA	Janes D.P., Patel H., Chantler P.D.;
DR	InterPro; IPR01609; myosin_head.	RT	Primary structure of myosin from the striated adductor muscle of the
DR	InterPro; IPR004009; Myosin_N.	RT	Atlantic scallop, Pecten maximus.;"
DR	InterPro; IPR002928; Myosin_tail.	RL	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR	Pfam; PF00612; IQ; 1.	DR	EMBL; AF34172; AAD2842.1; -.
DR	Pfram; PF00063; myosin_head; 1.	DR	HSSP; P2473; 1WDC.
DR	Pfam; PF02736; Myosin_N; 1.	DR	InterPro; IPR000048; IQ.
DR	Pfam; PF01576; Myosin_tail; 1.	DR	InterPro; IPR001609; myosin_head.
DR	PRINTS; PRO0193; MYOSINHEAVY.	DR	InterPro; IPR004009; Myosin_N.
DR	PRODOM; PD000355; myosin_head; 1.	DR	InterPro; IPR002928; Myosin_tail.
DR	SMART; SM00245; IQ; 1.	DR	InterPro; IPR002017; Spectrin.
DR	PROSITE; PS50096; IQ; 1.	DR	Pfam; PF00612; IQ; 2.
KW	MYOSIN.	DR	Pfam; PF00063; myosin_head; 1.
SEQUENCE	1933 AA; 221092 MW; CDF0CBAA475530F5 CRC64;	DR	PRINTS; PRO0193; MYOSINHEAVY.
Query Match	7.6%; Score 181; DB 13; Length 1933;	DR	SMART; SM00242; MYSC; 1.
Best Local Similarity	19.9%; Pred. No. 0 088;	DR	PROSITE; PS50096; IQ; 1.
Matches	99; Conservative 91; Mismatches 170; Indels 138; Gaps	DR	SMART; SM00245; IQ; 1.
Qy	31 LOCLTOWFENAPSRCPQCPIQVGGKKIINKFFDLAQEENVLDD--AEFLKNELDS 85	DR	PRINTS; PRO00355; myosin_head; 1.
Db	1142 LEEISERLEEAAGGATAAQIENKKREAFQKMRDL---EESTLOHETAAALKRQADS 1198	DR	PRODOM; PD000355; myosin_head; 1.
Qy	86 VKAQLSQK-----DREKRSQAITDLRDLEERNAVATESQNALNKAEMCST 134	DR	HSSP; P2473; 1WDC.
Db	1199 V-AELGEQIDNLQRQKOKLEKEKPFKEVKTMEIDL-----SSNMEAVALAKGNLKCR 1250	DR	InterPro; IPR001609; myosin_head.
Qy	135 LKKOMKFLEQRODTEKQAREEAHLLACKMKT-----MEDIELL----- 172	DR	InterPro; IPR004009; Myosin_N.
Db	1251 LEDQSEIKAKSNDENSRLQNDMAQRARLQTENGFSRQLEEKEALVSQLTRGKQAFTOQ 1310	DR	InterPro; IPR002928; Myosin_tail.
Qy	173 LOSRSEVEENIRDMGVQGOSAVEQALVYCVSLSKKEVENLKEAR-----KATGELAD- 223	DR	InterPro; IPR002017; Spectrin.
Db	1311 IEDLKRHVVEEVAKKALAHAVOSARHCDLIREQYBEEOEAKELORGMSKANSEVAQ 1370	DR	Pfam; PF00612; IQ; 2.
Qy	224 -----R-LKKDLVSSRSKLTNLTE--LDQAKLERLSAQDL-- 257	DR	Pfam; PF02736; Myosin_N; 1.
Db	1371 RAKYETDAIRTEELLEESKIKLALQRLQDAEESIEAVNSCASLEKTRKQRLQSEVEDLMID 1430	DR	PRINTS; PRO0193; MYOSINHEAVY.
Qy	258 -----QSADQITSLSRKSDSPPGNEILPASATNETPSRLVESPAPVE- 300	DR	SMART; SM00245; IQ; 1.
Db	1431 GERANALAANLKKQRNFQKLADWKQKYEVSQAELAQRKEARSLSTELFKMKNSEE 1490	DR	PRINTS; PRO00355; myosin_head; 1.
Qy	301 -----MINPRLHOPPEDEIDDLNTTFDVNTPTPSQHCLPK-----K 340	DR	SMART; SM00242; MYSC; 1.
Db	1491 LDHLETLKRNKNLQQ---EIS----DLSEQLGETGKSHETERAKTVSEKAIQ 1540	DR	PRINTS; PRO00355; myosin_head; 1.
Qy	341 LCLERARSPPQVNLLKVKHKSKPESOLSLSGQRCVQELDEELAGAFLFIRNA- VLGQK 398	DR	SMART; SM00245; IQ; 1.
Db	1541 TALEEEAGTLEEHESKILVQOLENLNOVSKFIDRKLAKEDEM---EQIKRNSQRVDLM 1596	DR	PRINTS; PRO00355; myosin_head; 1.
Qy	399 QPNRTTAESSTDVAR1 416	DR	SMART; SM00242; MYSC; 1.
Db	1597 Q-STLDESEVRSRNDALRV 1613	DR	PRINTS; PRO00355; myosin_head; 1.
RESULT	30	SEQUENCE	1940 AA; 223141 MW; A3D09DCBEB16F90 CRC64;
Q9U/P3		Query Match	7.6%; Score 181; DB 5; Length 1940;
ID	0907E3	Best Local Similarity	23.0%; Pred. No. 0 088;
AC	0907E3; PRELIMINARY; PRT; 1940 AA.	Matches	101; Conservative 67; Mismatches 125; Indels 146; Gaps
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)	Qy	55 KKTINKLFD--LAQEENVLDAEFLKNELDSVK-----AQLSQ 92
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)	Db	906 EKLINQKADPESOTKRELEERLLDEEADALEGIGKKMETDANSNLLKDGIDLENTLQAE 965
DE	MYOSIN HEAVY CHAIN.	Qy	93 KDERKRSQAIIDIT-----RDTLEERNATVLSQ-----NALNKA 128
OS	Pecten maximum (King scallop) (Pilgrim's clam).	Db	966 QDKAHKDNO--ISTLQGEMAQQDEHIGKLNEKEKKALEANKKTSLSQAEEDKCNHLNK- 1022
OC	Bukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Pectinoidea;	Qy	129 EMICSTLKKMFLEQRODTEKQAREEAHLLCKK-----TMEDIELLQSQREVEEM 183
OC	Pectinoidea; Pectinidae; Pecten.	Db	1023 -LKAKLEQALDELEDDLNLEREKKVFGDVEKAKRVQEDLQSTOENEDLVERK-ELEEN 1079
NCBI-TaxID	6579;	Qy	184 IR-----DMGVGQGOSAVEQALVYCVSLSKKEVENLKEAR-----KATGELAD- 232
[1]		Db	1080 VRKKEAELSTLNKLEDEONLVSQLOQKVKELOQARIEELLEEARNAKRAVEKORAEI 1139
RESULT	31	Q9U/P3	DR
ID	0907E3	Query Match	7.6%; Score 181; DB 5; Length 1940;
AC	0907E3; PRELIMINARY; PRT; 2007 AA.	Best Local Similarity	23.0%; Pred. No. 0 088;
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)	Matches	101; Conservative 67; Mismatches 125; Indels 146; Gaps
DT	01-NOV-1996 (TREMBlrel. 01, last sequence update)	Qy	335 HCLPKKLCLERARZPMQNVLKVKVKVKSKPESOLS-----LGQCVGELDEELAGAFL 388
DE	MYOSIN HEAVY CHAIN.	Db	1199 -----ANAMEDQV-----DQLQKVSKLE-----DKDKIREMD----DIESQWT 1236
OS	Pecten maximum (King scallop) (Pilgrim's clam).	Qy	1237 HNMKNKGCGEK-----VMQF-----ESQMSDLNARLEDSQRSINEL----- 1273
OC	Eukaryota; Metazoa; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	Db	389 FIRMVNLGKQPNRTAES 407
OC	Gallus gallus (Chicken).	Qy	1274 -----QSQSKLQAE 1284

OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 SEQUENCE FROM N.A.; PubMed=1355479;
 RX MEDLINE=92388144; PubMed=1355479;
 RA Takahashi M., Kawamoto S., Adelsrein R.S.;
 RT "Evidence for inserted sequences in the head region of nonmuscle
 myosin specific to the nervous system. Cloning of the cDNA encoding
 the myosin heavy chain-B isoform of vertebrate nonmuscle myosin.";
 RL J. Biol. Chem. 267:17864-17871(1992).
 DR EMBL; MG3676; AAA8986_1; -.
 DR EMBL; MG3676; AAA8985_1; -.
 DR EMBL; MG3676; AAA8988_1; -.
 DR HSSP; P10587; 1BR2;
 DR InterPro; IPR000008; IQ;
 DR InterPro; IPR001609; IQ;
 DR InterPro; IPR04009; myosin_head.
 DR InterPro; IPP002938; Myosin_tail.
 DR InterPro; IPR02017; Spectrin.
 DR Pfam; PF00063; myosin_head; 2.
 DR Pfam; PF02736; Myosin_N; 1.
 DR Pfam; PF01576; Myosin_tail; 1.
 DR PRINTS; PRO0193; MYOSINHEAVY;
 DR PRODOM; PD000355; myosin_head; 1.
 DR SMART; SM0042; MYSC; 1.
 DR PROSITE; PS50096; IQ; 1.
 DR SEQUENCE 2007 AA; 232592 MW; 36A591368CD264BA CRC64;

Query Match 7.6%; Score 181; DB 13; Length 207;
 Best Local Similarity 21.5%; Pred. No. 0.091; Gaps 16;
 Matches 96; Conservative 87; Mismatches 167; Indels 96; Gaps 16;
 Qy 68 QEBENVLDAEFLKNEELDSVKAQLSQOKREKRSQDQAIIITDLSLEERNATIVESLQNALNK 127;
 Db 1536 QNKOLRADMEMLMSKDKDVGKVNHELESKR-----TLEQVEEMTQOLEEDELQO 1588
 Qy 128 AEMLCSTIKKOMFKLEQDQETDQAREAAHLKCKM-KTMEQIELLIQSQRSE----- 179.
 Db 1589 TEAKKLRLVNMQAMKAQFERDIQARDEPNEEKRMVLYQVRSLAELEDERKORALAVA 1648
 Qy 180 ---VEEMTRDMGVGQ-----SAVEQOLAVCVSLLKEYENLKEARKATEBLADRUK 226
 Db 1649 AKKKMEMDLKDLEQKIERANKARDEA1KQLRQLQAQMDYORBLEEARSRDIBAQS 1707
 Qy 227 KDVYSSRLKLTNTLEDOAKLERSACKDQADQETSLRKSKDDPGNLPASATNE 286
 Db 1708 E---SEKKLGIEAIHQLOQEFAASERARRHAEQERDEL---ADEIANSASSGKSLID 1760
 Qy 287 TVSL-----VFESPAPEVMMPRLHQPPGDEIDLNLNTFDWVNPPTGSGHC 336
 Db 1761 EKRLLEARIAOLEEELEFOSSHNLNLERFRK-----TTLQVDPLNSLAGESA 1810
 Qy 337 LPKKCLCERARSQPNVVKHV KVSKPQLSQLGGQRCVGELDEELAGAFPLFIRNAVL 395
 Db 1811 AQKS---ENARQQLERONKELKAKLQLELEGSVSKFKATISTLEAKIAQL----- 1857
 Qy 396 GQKOPNRNTAESAESSSTDVYRIGPDGLGRK-----FIOPRI---TPIIRPVPKA 445
 Db 1858 -EEOLEOEAKERAAANKLVR-----RTEKKLUKEVFMQVEDERRHADQYQKOMEKANA 1908
 Qy 446 KSKOKVR-----IKTVSSASPKL 464
 Db 1909 RMKQLKROLEEEAEEATRANASRRKL 1934

RESULT 32
 ID 096720 PRELIMINARY; PRT; 692 AA.
 AC 096720; DR 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE PARAMOSIN-LIKE ALLERGEN (FRAGMENT).
 OS Dermatophagoïdes fariné (House-dust mite).
 OC Eukaryota; Metazoa; Arthropoda; Chelicera; Arachnida; Acari;
 OC Acariformes; Sarcoptiformes; Astigmata; Analgoidea; Pyroglyphidae;
 OC Dermatophagoïdes.
 DR EMBL; MG3676; AAA8986_1; -.
 DR HSSP; P10587; 1BR2;
 DR InterPro; IPR000008; IQ;
 DR InterPro; IPR001609; IQ;
 DR InterPro; IPR04009; myosin_head.
 DR InterPro; IPP002938; Myosin_tail.
 DR InterPro; IPR02017; Spectrin.
 DR Pfam; PF00063; myosin_head; 2.
 DR Pfam; PF02736; Myosin_N; 1.
 DR Pfam; PF01576; Myosin_tail; 1.
 DR PRINTS; PRO0193; MYOSINHEAVY;
 DR PRODOM; PD000355; myosin_head; 1.
 DR SMART; SM0042; MYSC; 1.
 DR PROSITE; PS50096; IQ; 1.
 DR SEQUENCE 2007 AA; 232592 MW; 36A591368CD264BA CRC64;

Query Match 7.5%; Score 180; DB 5; Length 692;
 Best Local Similarity 21.9%; Pred. No. 0.034; Gaps 13;
 Matches 87; Conservative 64; Mismatches 160; Indels 86; Gaps 13;
 Qy 59 INKLFEDLAQEEENVL-DAEFLKNEELDSVKAQLSQOKREKRSQDQAIIITDLSLERNA 116
 Db 104 INRVIETLHKQRLSQETVELIK-EVHEVKLQDNANHLKTQIAQQLEDTHRLEER 162
 Qy 117 TVESLQNALNKAEMLCSTIKKOMFKLEQDQETDQAREAAHLKCK---MKIMEQEL 171
 Db 163 KRASLENHARTLEVELESJKVOL-----DESEARBLELERQQLTAKANGDAASWKSKYE 215
 Qy 172 LQQSRSEFEEMTRDMGVG---OSAVEOLAVCVSLLKEYENL-----EARKTG 219
 Db 216 ELQAHADEVEELRKMAQISEVEBQELLNKCSLRSRQSEVEFLIMOLEKAR 275
 Qy 220 ELAD-----RLKDLVSSRLKLTNTLEDOAKLERSACKDQADQETSLRKSKDD 273
 Db 275 HAQZLEKRAVQALEKINLDKLNKLEEVMTMQAKELRKVIAELOQHBEYKLQDQD 335
 Qy 274 PPGNLEPASATNETVSLRVFESPAPVEMMPRLHQPPGDEIDLNLNTFDWVNPPTGSGS 333
 Db 335 -----LARENKKLTDAAEKSQINDAHRRIE---QEIEKR----- 370
 Qy 334 QHCLPKKLQLEERASPMQMVNLKVHVKSPLGSQSLGGRCVGIL-----D 379
 Db 371 -----LENERDELSAYKEETLRQEEAKN---ORLIAALAQVRYDYERKLAQD 418
 Qy 380 EELAGAFFPIFIRNAVLGQKOPNRNTAESAESSSTDVRI 416
 Db 419 EEEIALRKQY-QTEIEOLNMRЛАЕААКЛТЕАRL 453

RESULT 33
 Q21440 ID Q21440 PRELIMINARY; PRT; 1992 AA.
 AC 021440; DR 01-Nov-1996 (TREMBrel. 01, Created)
 DT 01-Nov-1996 (TREMBrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)

QY	336	CILPKKCLLERARSPHONVLKVHKVKPSQSLGGORCVGELDELAGAFPLFIRNA--	393
Db	702	--ALERESTLEHEESKILRVOLEMLNQVKSEIDRKLAEDKEI---EQIKRNSQR	751
QY	394	VLGKQKPNRTAESNSSTDWVRI	416
Db	752	VMDNQ-STUDSETRSNDLRY	773
RESULT	37		
Q26080			
ID	026080	PRELIMINARY;	PRT; 1950 AA.
AC	026080;		
DT	01-NOV-1996 (TREMBREL. 01, Created)		
DT	01-NOV-1996 (TREMBREL. 01, Last sequence update)		
DE	MYOSIN HEAVY CHAIN		
OS	Placopecten magellanicus (Sea scallop).		
OC	Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea; Pectinidae; Pectinidae; Placopecten.		
OX	NCBI-TAXID=6577;		
RN	[1]	SEQUENCE FROM N.A.	
RC	TISSUE=ADUCTOR MUSCLE;		
RA	Perrault-Micelle, C.; Kalabokis V.; Nyitrai, L.; Szent-Gyorgyi A.G.;		
RT	"Sequence variations in the surface loop near the nucleotide binding site modulate the ATP turnover rates of molluscan myosins.";		
JL	Muscle Res. Cell Motil. 0:0-0(1996).		
EMBL:	US9295; AAB03661.1; -		
HSSP:	P24733; IWCDC		
DR	InterPro: IPR00048; IQ.		
DR	InterPro: IPR01609; myosin_head.		
DR	InterPro: IPR00409; Myosin_N.		
DR	InterPro: IPR02928; Myosin_tail.		
DR	InterPro: IPR02017; Spectrin.		
DR	Pfam: PF00612; IQ; 2.		
DR	Pfam: PF00063; myosin_head; 1.		
DR	Pfam: PF02736; Myosin_N; 1.		
DR	Pfam: PF01576; Myosin_tail; 1.		
PRINS:	PR00193; MYOSINHEAVY		
PRODOM:	PD00035; myosin_head; 1.		
SMART:	SM00015; IQ; 1.		
SMARF:	SM00242; MYC; 1.		
PROSITE:	PS50096; IQ; 1.		
SEQUENCE	1950 AA;	224184 MW;	6FE358802352C19A CRC64;
Query Match	7.5%	Score 179; DB 5; Length 1950;	
Best Local Similarity	21.9%	Pred. No. 0.11; Mismatches 134; Gaps 18;	
Matches	95;	Conservative	70; Mismatches 134; Indels 134; Gaps 18;
QY	55	KKTINKLFFD-LAQEEENVLADEFKLNEFLDSVK-----AOLSO	92
QY	905	EKLIMQKADFEQIKELEERFLDEDAASDLEGIGKKMMEGDNNANLKKDIELEHSLOKE	964
QY	93	KDREKRDSQAAIDDL-----RPTLEERN-ATVESLO-----NALNKA	128
Db	965	QEKAHKDNO-ISTLQGEMSQDHEHIGKLNEKEKALEANKKTSDSLQABEDKCNHLNK-	1021
QY	129	EMLCSTLKKQMFQLEQDTEKQAREEAKFLCKMK----TMEQIELLQSQRSEVEEM	183
QY	1022	--EKAKLEGAIDLEDNLREERKVKRGDVKEAKSKVQEQLKSTQENVEDLERVKR-ELEEN	1078
Db	184	IR-----DMVGSGSAVEQALAVYCYSVKKEYENTKEARKATGELADRKLKDVLSS	232
QY	1079	VRRKEAEITLNSKLEDEQNLNSOLQRKIKELQARIELEELAEARNASKVERAEL	1138
QY	233	RSKIKLTNLNEDO-----KELRSAQDKDQA---DQETSLRKSDP	274
Db	1139	NRELEELGERLDEAGGATSAQIELNKKRELLKIRTRDLEASLQEAQISAIKKHD-	1197
QY	275	PGNLEPASITNEYSLVLFESPAPVEMMRPLHOPFGEGIDLNTPPPQTGSQHCLPK--KLC	342
RESULT	39		
Q63731			
ID	Q63731	PRELIMINARY;	PRT; 1999 AA.
AC	Q63731;		
DT	01-NOV-1995 (TREMBREL. 01, Created)		
DT	01-NOV-1995 (TREMBREL. 01, Last sequence update)		
Db	1273	--QSQSRQLAQEN	1283
Db	1198	--AANEMADDOV--DQLOKVKSEKENNKMSENEDELQOI-----Q	1235
QY	335	HCLPKKCLLERARSPHONVLKVHKVKPSQSLGGORCVGELDELAGAFPLFIRNA	394
Db	1236	HISKNGCSEKYMKQFES-----QVSDLNARLE-DSORSINEL-----	1272
QY	395	LGOKQPIRTAES 407	
Db	1273	--QSQSRQLAQEN	1283
RESULT	38		
Q9BWGO			
ID	Q9BWGO	PRELIMINARY;	PRT; 471 AA.
AC	Q9BWGO;		
DT	01-JUN-2001 (TREMBREL. 17, Created)		
DT	01-JUN-2001 (TREMBREL. 17, Last sequence update)		
DT	01-DEC-2001 (TREMBREL. 19, Last annotation update)		
DE	HYPOTHETICAL 54.6 kDa PROTEIN (FRAGMENT).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrini; Hominidae; Homo.		
OX	NCBI-TAXID=9606;		
RN	[1]	SEQUENCE FROM N.A.	
RP	RC	TISSUE=EYE, RETINOBLASTOMA;	
RA	Strausberg R.;		
RT	Submitted (Nov-2000) to the EMBL/GenBank/NCBI databases.		
RL	EMBL: BC000280; AAH0280.1; -		
DR	InterPro: IPR00228; Myosin_tail.		
DR	InterPro: IPR00533; Tropomyosin.		
DR	Pfam: PF01576; Myosin_tail; 1.		
DR	PRINTS: PR00194; TROPOMYOSIN.		
KW	Hypothetical protein.		
FT	NON_TER	1	
SQ	SEQUENCE	471 AA;	54589 MW;
Query Match	7.5%	Score 178.5; DB 4; Length 471;	
Best Local Similarity	22.0%	Pred. No. 0.027; Mismatches 136; Indels 55; Gaps 7	
Matches	75;	Conservative	75; Mismatches 136; Indels 55; Gaps 7
QY	75	DAEFLKNELDSYKAQOSQDKRDRDSQAIIDTLRDTFERNATVSESIONALNKAEMCST	134
Db	135	LKKQMKLQEORODE-----TKQAREEAKRICKMK-----TMEQIELLOSORS	178
QY	67	DAEFLKNELDSYKAQOSQDKRDRDSQAIIDTLRDTFERNATVSESIONALNKAEMCST	126
Db	67	MKAQFENDLQDPEQNEERKKRLLKQYRELEERKORALAVAKKKMEDIKKOLEA	126
QY	179	EVE-EMTRDMGVGQSAVEQALAVYCYSVKKEYENLKEARKATGELADKLVLVSSRSKL	236
Db	127	QIAAARKARD-----EVTKQLKQLQROMKDYRELEBARASRDEIFQSKO-----SEKKL	177
QY	237	KYLNTLFLDQAKLELRSLAQDKDQADQETSLRKSDPQNLPESATNETVSR-----	291
Db	178	KSLEAETLQLQBELASSEERRARRHAEQERDEL---ADELTNSASGKSLDDEKKRLEARIA	234
QY	292	-----VFPESPAVEMMPRLHOPFGEGIDLNTPPPQTGSQHCLPK--KLC	342
Db	235	QLEEEELFEEQSNMELLNDRFK-----TTLQYDNTLNAELAERSAQQSDNARQ	284
QY	343	LERARSPMQNVKKVHKVKPSQSLGG-ORCVGELDEL	382
Db	285	LERQNKLAKLQELGCAVSKSFKATISALEAKIGQLEQL	325

Db 172 LPTCPVCLERMDESVDGVLTILCNHAFHASCLMKWGDSD---TCPVCRHVQTPGLVEDSV 227
 Qy 51I QWQKTTI-----INK 61
 Db 228 CMECIGTDSLWICLICGHVGCGRYOGGHAAHFRATNHTFAMQJGTSSTWDYASDNFVR 287
 Qy 62 LFFDLAQEEENVLDAAEFLKNELDSVKAQLSQDREKRSQDQAIDTLRDTLEERNATESVL 121
 Db 288 LF-----ONKSOCKLV-----ASQPEKD-----EREKIDS 314
 Qy 122 QNALKAEMTCSTLUKKQMFKLERQRODETKOA---REEAHLRKCRMKTMBQIEELLQSOR 177
 Db 315 Q-MEFTYLITSLQDITQRYEYERMERLEOEWNHKATANDAKTEVSELQOLQOONMQEK 372
 Qy 178 SEVEEMIRDMVGQSAVEQAVYCUSLKEYENLKEARRATGEADRLKKDLSSRSKUK 237
 Db 373 VNLE-----RKLAQHTAKLKDVQKQNEER-----ELSKALQNSNOSSWHGKTK 415
 Qy 238 TINTELDQAKLERSAQKDLQSADEITSURKSKDD-----PPGNLEPASATNETV 288
 Db 416 LLEQDYNEFK-----QTHDAEVTELKEQRLDIMFFLDNQQLANTEAGG---TV 462
 Qy 289 SRLVESPAP 298
 Db 463 TGIAEKEPDP 472

Search completed: September 4, 2002, 16:15:58
 Job time: 1482 sec